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Simulating the Spread of an Outbreak of Foot and Mouth Disease in California

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THESIS

SIMULATING THE SPREAD OF AN OUTBREAK OF FOOT AND MOUTH DISEASE IN CALIFORNIA

by

Brian S. Axelsen

June 2012

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13. ABSTRACT (maximum 200 words)

Foot and mouth disease (FMD) is a highly contagious viral disease affecting cloven-hoofed domestic and some wild animals. A hypothetical outbreak of FMD begun in California was recently estimated to have a national impact of up to $55 billion, mostly due to international trade restrictions (Carpenter, O'Brien, Hagerman, & McCarl, 2011). Therefore, preparedness for an outbreak is a high priority within the livestock industry, and state and federal government.

We use simulation and a designed experiment to identify robust governmental and industrial surveillance response strategies to control the spread of FMD. A strategy is considered robust if it is effective across a number of outbreak scenarios and a variety of disease spread characteristics.

The main contributions of this thesis are: (1) the development of FMD outbreak scenarios across California that can be used in conjunction with a state-of-the-art, animal disease simulation model, and (2) the development and analysis of an efficient experimental design that allows for the identification of key parameters affecting the spread and containment of an FMD outbreak.

The analysis of over 400,000 simulations in the experimental design indicates two key areas for the control ofFMD:

(1) surveillance activities at dairy and dairy-like premises are a dominant factor in early identification of the disease and increased surveillance leads to lower impacts of an outbreak; and (2) fast initial response and capacity of depopulation resources are also key factors in controlling an FMD outbreak, even when no preemptive depopulation strategies are considered.

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SIMULATING THE SPREAD OF AN OUTBREAK OF FOOT AND MOUTH DISEASE IN CALIFORNIA

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ABSTRACT

Foot and mouth disease (FMD) is a highly contagious viral disease affecting cloven-hoofed domestic and some wild animals. An A hypothetical outbreak of FMD begun in California was recently estimated to have a national impact of up to $55 billion, mostly due to international trade restrictions (Carpenter, O'Brien, Hagerman, & McCarl, Carpenter et al., 2011). Therefore, preparedness for an outbreak is a high priority within the livestock industry, and state and federal government.

We use simulation and a designed experiment to identify robust governmental and industrial surveillance response strategies to control the spread of FMD. A strategy is considered robust if it is effective across a number of outbreak scenarios and a variety of disease spread characteristics.

The main contributions of this thesis are: (1) the development of FMD outbreak scenarios across California that can be used in conjunction with a state-of-the-art, animal disease simulation model, and (2) the development and analysis of an efficient experimental design that allows for the identification of key parameters affecting the spread and containment of an FMD outbreak.

The analysis of over 400,000 simulations in the experimental design indicates two key areas for the control of FMD: (1) surveillance activities at dairy and dairy-like premises are a dominant factor in early identification of the disease and increased surveillance leads to lower impacts of an outbreak, and (2) fast initial responsiveness response and capacity of depopulation resources are also a key factors in controlling an FMD outbreak, even when no pre-emptive depopulation strategies are considered.

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LIST OF ACRONYMS AND ABBREVIATIONS

AIC	Akaike Information Criterion
ANOVA	Analysis of Variance
ARP	At Risk Premises
Avg	Average
AHFSS	Animal Health and Food Safety Services
BZ	Buffer Zone
CA	Control Area
CalTrans	California Department of Transportation
CART	classification and regression trees
CCS83	California Coordinate System
CDFA	California Department of Food and Agriculture
CP	Contact Premises
DoD	Department of Defense
DOE	Design of Experiment
EPA	Environmental Protection Agency
FADD	Foreign Animal Disease Diagnostician
FADDL	Federal Foreign Animal Disease Diagnostic Laboratory
FEMA	Federal Emergency Management Agency
FIPS	Federal Information Processing Standard
FMD	Foot and mouth disease
FP	Free Premises
GAO	U.S. General Accounting Office
GIS	Geographic Information System
HSD	honestly significant difference
I/O	Input/Output
IP	Infected Premises
ISP	InterSpread Plus
IZ	Infected Zone

km	Kilometer
KSL	Kolmogorov-Smirnov-Lillefors
Lat	Latitude
LLNL	Lawrence Livermore National Laboratory
Long	Longitude
m	Meter
MESA	Multiscale Epidemiological/Economic Simulation and Analysis
MOE	measure(s) of effectiveness
MP	Monitored Premises
MPVM	Master of Preventive Veterinary Medicine
NAADSM	North American Animal Disease Spread Model
NAHLN	National Animal Health Laboratory Network
NASS	National Agricultural Statistics Service
NOLH	nearly orthogonal Latin hypercube
NSTC	National Science and Technology Council
OIE	WORLD ORGANISATION FOR ANIMAL HEALTH
QUADS	Quadrilateral countries (Australia, Canada, New Zealand, and the United States)
SEED	Simulation Experiments and Efficient Design
SP	Suspect Premises
SS	Sum of Squares
Std Dev	Standard Deviation
SZ	Surveillance Zone
U.K.	United Kingdom
U.S.	United States
USAHA	U.S. Animal Health Association
USDA	U.S. Department of Agriculture
VP	Vaccinated Premises
VZ	Vaccination Zone

EXECUTIVE SUMMARY

Foot and mouth disease (FMD) is a highly contagious viral disease affecting cloven-hoofed domestic and some wild animals. Most adult animals recover from the disease, but it debilitates them; leading to severely decreased meat and milk production. The economic impact on a country with an FMD outbreak can be extensive due to the cost of eradicating the virus, the secondary effects to local economies, and the international trade impact on all animal products that the country exports. For example, the 2001 outbreak of FMD in the United Kingdom led to the destruction of approximately 4 million animals at an estimated economic loss of $5 billion to the food and agriculture sector, and a comparable amount to the tourism industry (U.S. General Accounting Office [GAO], 2002). Even though the United States has been free of this disease since 1929, the Executive Office of the President, Office of Science and Technology Policy has listed FMD as one of four animal diseases that are "high priority threats" in its Research & Development Plan for 2008–2012 (National Science and Technology Council [NSTC], 2007).

We study the spread of FMD in California using a specifically designed herd-based, disease-spread simulation software package and an efficient design of experiment (DOE) to explore a number of "what-if" scenarios of FMD outbreaks in California. The software package, called InterSpread Plus (ISP), has been used extensively to model outbreaks of this disease in modern livestock countries including the United Kingdom, Republic of Korea, and New Zealand.

Our research makes two major contributions to the study and modeling of FMD in California. First, we undertake a significant data development effort to use a state-of-the-art animal disease simulation, ISP, to analyze potential FMD outbreaks in California. This data will allow future researchers to study alternative scenarios and control strategies as they are developed. Second, we develop an efficient DOE, which allows us to explore 26 disease-spread factors and 46 response factors across 8 outbreak scenarios, using hundreds of thousands of simulations, as opposed to a naive strategy that

would require more than trillions (2^{73}). In this way, we can perform simulation analysis of the output to identify the relevant disease and control factors for the spread of FMD in California

The two major results for the control of FMD, as indicated by our analysis, are:

- The most important disease surveillance is done at dairy and dairy-like facilities, or premises. We see that the surveillance parameters of these premises are the dominant control factors in both decreasing the detection time and decreasing the size of the outbreak. This is likely because these types of premises usually have personnel on staff who have daily contact with their animals and because the clinical signs of infection in cattle are generally easier to detect than in other species. These characteristics lead to decreased time until detection, which leads to quicker implementation of controls and smaller outbreaks. Continued research into how to make this type of surveillance as efficient as possible could have a significant impact on the size of an outbreak if it ever occurs in California.
- The size and responsiveness of depopulation resources play a significant role in decreasing the size of outbreaks. This is surprising, because our models do not use preemptive depopulation. Instead, the model only depopulates detected premises. The analysis confirmed that depopulating infected premises quickly and significantly limited the spread of the disease. This requires the availability of large amounts of resources in a timely manner. The analysis suggests that if the state does not plan on using preemptive depopulation, then depopulation resources should be readily available on very short notice to facilitate the rapid control of an FMD outbreak.

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As I come to the end of this thesis, I do so with a humble heart, knowing that it was not my talents alone that produced this document. Many people added their time, talents, expertise, and support to get me through this process, and I am grateful.

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I. INTRODUCTION

A. PURPOSE

Foot and mouth disease (FMD) is a highly contagious viral disease affecting cloven-hoofed domestic and some wild animals. The United States has been free of this disease since 1929, but preparedness for an outbreak is a high priority within the livestock industry, and state and federal government. The Executive Office of the President, Office of Science and Technology Policy has listed FMD as one of four animal diseases that are "high priority threats" in its Research & Development Plan for 2008–2012 (National Science and Technology Council [NSTC], 2007, p. 5). This document goes on to state that:

> An incursion of FMD within U.S. borders could result in severe disruption of the dairy, cattle, and swine industries and allied sectors, the loss of export markets, and stop movement restrictions that would create significant disruption to the national economy (including transportation systems, travel, and consumer confidence).

FMD is a top priority for the state of California in particular. According to the 2010 Census of Agriculture, California is ranked #1 in dairy production and #4 in beef production in the United States. The combined market value of these two industries is $9.1 billion annually (United States Department of Agriculture National Agricultural Statistics Service [NASS], 2010). An outbreak of FMD is a large potential threat to these industries in terms of both their health and economic productivity (Hagerman, McCarl, Carpenter, & O'Brien, 2009). The California Department of Food and Agriculture (CDFA) lists FMD as one of two animal diseases that are "potential emergencies" within the state. The CDFA's Animal Health and Food Safety Services Division (AHFSS) maintains several websites devoted to the disease, including general information about the disease, livestock producer guides to preventing and reporting suspected occurrences of FMD, and emergency preparedness guides in case of an outbreak.

Because the disease spreads so quickly, authorities tasked with controlling the outbreak must move aggressively to implement control measures to stop its geographic expansion. What measures they implement and how they are implemented can have

tremendous impacts on both local and state economies. For example, if movement restrictions are applied to too small an area, the disease may spread outside of the controlled area and cause a larger outbreak. If, however, they are applied to an overly large area, it may cause undue collateral damage because all industries in those controlled areas suffer economic hardship either directly (e.g., to farm revenue due to depopulation of infected premises), or indirectly (e.g., to small business revenue due to movement restrictions).

Our research uses simulation and a designed experiment to attempt to determine robust governmental and industrial surveillance and response strategies across a number of outbreak-starting scenarios and considers a variety of disease-spread parameters. We hope to provide insight to policy makers so that they can be prepared if, and when, an outbreak occurs in California.

B. BACKGROUND

FMD is extremely contagious and difficult to control. Its most significant impact is generally on cattle and swine, although it also affects sheep, goats, deer, and several other, mostly cloven-hoofed, animals. The virus can be spread by animals, people, inanimate objects, or by aerosol. It is a moderately robust virus that can persist for weeks or months given neutral pH and favorable environmental conditions. There are seven distinct serotypes of the virus along with many more subtypes of each serotype. Any vaccine used must be specific to the type and subtype of the virus in order to be most effective. The symptoms of the disease vary in severity with serotype and species infected, but FMD is generally characterized by a fever and painful blister-like lesions in the mouth, on the tongue and lips, between the hooves, and on the teats of an infected animal. Most adult animals recover from the disease, but it debilitates them, which leads to severely decreased meat and milk production. FMD is not zoonotic, which means that it is not transmittable to humans under natural conditions; however, it does indirectly affect the health of nearby human populations through increased incidence of clinical

depression, posttraumatic stress, and suicides due to the emotional and economic impacts of rapid and large-scale depopulation of animals that is sometimes needed to control historic outbreaks (United States Animal Health Association (USAHA), 2008).

The economic impact on a country with an FMD outbreak can be extensive due to the cost of eradicating the virus, the secondary effects to local economies, and the international trade impact on animal product exports. The trade impacts could be particularly expensive for the United States because all nonpasteurized animal products for the entire country would be restricted under international trade rules. Therefore, an outbreak of FMD in California would impact non-infected states such as Iowa and Missouri, where there is a large pork products exporting industry. The United States (U.S.) has not had an FMD outbreak since 1929, but a recent study funded by the Department of Homeland Security estimated that an outbreak begun in California could have a national impact of up to $55 billion if the disease was not detected for 21 days, which was the detection delay in the United Kingdom (U.K.) in 2001 (Carpenter et al., 2011). That outbreak of FMD in the U.K. led to the destruction of approximately 4 million animals, at an estimated economic loss of $5 billion to the food and agriculture sector, and a comparable amount to the tourism industry (U.S. General Accounting Office [GAO], 2002).

C. CURRENT PREVENTION AND RESPONSE STRATEGIES AGAINST FMD

Mainly due to the potential economic impact of FMD on the country, the U.S. government has developed a plan to prevent and control (if necessary) an outbreak of this disease. This plan can be divided into several parts: prevention, detection, selection of a control strategy, and management of the control strategy.

1. Prevention

Outbreaks of FMD are constantly occurring globally and the disease is endemic in many parts of the world (see Figure 1). The USDA is the lead government organization charged with protecting the country from foreign animal diseases, and it utilizes a multilayered defense. The first layer is outside of our borders, where they conduct

multinational outbreak response exercises, monitor reported outbreaks, provide monetary and expert resources to affected countries, and help to set up FMD control zones in regions such as Central and South America. The USDA's next layer is at the national borders, where it works alongside U.S. Customs to implement preventative measures for international passenger and cargo traffic, livestock and animal product imports, international mail, and garbage from international carriers. U.S. efforts to protect itself have been effective for over 80 years, but the magnitude and volume of legal and illegal people and products crossing our borders means that the country is still vulnerable to the disease.

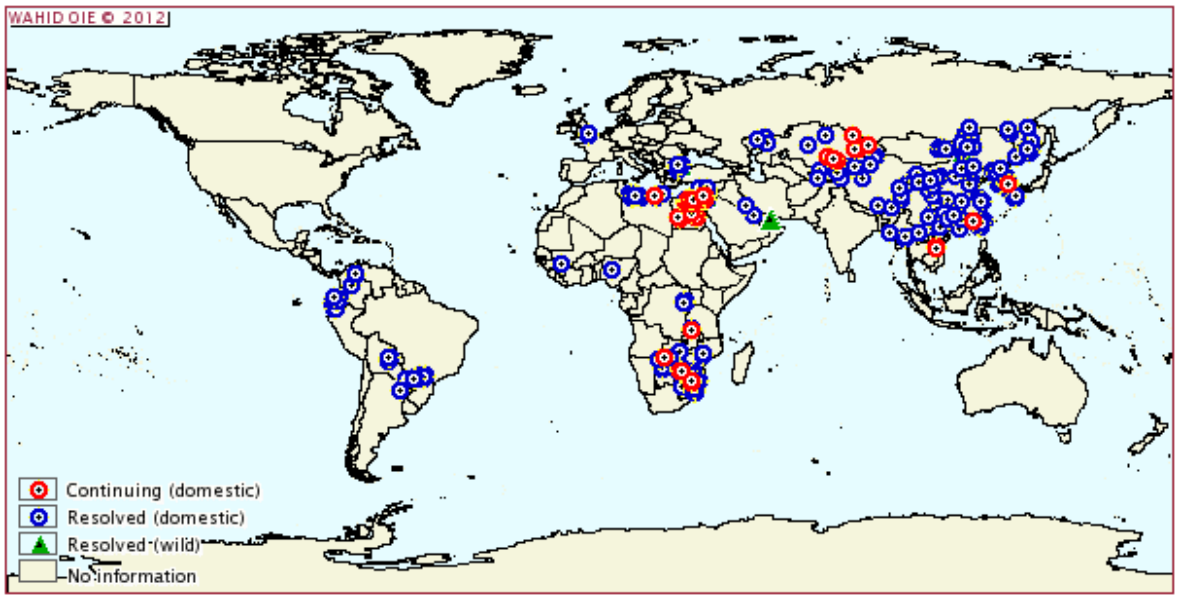

Figure 1. FMD outbreaks after 2005 (OIE, 2012)

2. Detection

If FMD is detected within the U.S., the federal government, as well as most state governments, has developed and tested emergency response plans. At the federal level, the Federal Emergency Management Agency (FEMA) would coordinate the response and the USDA would be the lead agency. Some of the more than 20 federal agencies involved would be the Department of Defense (DoD) to provide personnel, equipment and transport; the Environmental Protection Agency (EPA) to advise on the disposal of

animal carcasses; and the National Park Service to advise on susceptible wildlife management. Since this thesis applies specifically to an outbreak of FMD in California, we focus on California's, as well as the USDA's, response plans.

The initial indication of an FMD outbreak will most likely come from a private veterinarian called by, or on the staff of, a livestock owner who notices unusual patterns of sick animals or significant production losses. The veterinarian is required by law to report a suspected case of FMD to the CDFA. A government agency, such as the Food and Drug Administration, the USDA, or U.S. Customs may also originate a report. Upon notification, the CDFA contacts the USDA and dispatches a Foreign Animal Disease Diagnostician (FADD) to collect samples and classify the diagnosis as "unlikely," "possible," or "highly likely." For the first two scenarios, the FADD orders the livestock facility to stop all animal movement until lab results rule out FMD. In the event of a diagnosis of "highly likely" by the FADD, the State Veterinarian places a State Quarantine on the facility, establishes an appropriate movement control area around the premises, and directs that all contacts to the facility be traced back to an appropriate point in time. The FADD then works with the facility to ensure that proper biosecurity measures are implemented. In all three scenarios, the FADD sends the sample to an approved National Animal Health Laboratory Network (NAHLN) lab for further evaluation, with the conformational diagnosis being made by the Federal Foreign Animal Disease Diagnostic Laboratory (FADDL) at Plum Island, New York.

3. Selection of a Control Strategy

Once FMD is confirmed by USDA, the CDFA and USDA select response strategies to use within the control areas. These responses could include one of or a combination of the following:

- *Stamping-Out*, which would depopulate all infected premises, contact premises, and at-risk susceptible animals;

- *Stamping-Out with Emergency Vaccination to Slaughter*, which modifies the Stamping-Out response by vaccinating at-risk susceptible animals prior to slaughtering or depopulating them;
- *Stamping-Out with Emergency Vaccination to Live*, which is the same as *Stamping-Out with Emergency Vaccination to Slaughter* except that the vaccinated animals would be allowed to live out their useful lives; or,
- *Emergency Vaccination without Stamping-Out*, which is highly unlikely to be used during an initial outbreak, but may be used if the disease becomes widespread and resources to stamp-out do not exist.

The selection of one or a combination of these responses is based on the scale and circumstances of the outbreak. For example, Stamping-Out is most appropriate to a well-contained region where the probability of spreading beyond the region is low and the resources to depopulate and dispose of the animals are readily available. Whereas, Stamping-Out with Emergency Vaccination to Live may be most appropriate where public opinion is opposed to slaughtering uninfected animals, or where there is a need to protect high value genetic stock, facilities that have long-lived production animals, or a high density population of high risk susceptible animals.

4. Management of the Control Strategy

The USDA has several designations for specific locations in the event of an FMD outbreak in order to better manage the response to the outbreak. The responses listed above may be used at any of these designated locations. *Premises* are the smallest designation and identify, among others:

- *Infected Premises (IP)*, where a presumptive positive or confirmed positive case exists;
- *Contact Premises (CP)*, where susceptible animals may have been exposed either directly or indirectly to FMD;
- *Suspect Premises (SP)*, which is under investigation due to the presence of susceptible animals reported to have clinical symptoms similar to FMD;

- *At-Risk Premises (ARP),* which have susceptible animals, but none of those susceptible animals have clinical signs compatible with FMD;
- *Monitored Premises (MP),* which objectively demonstrate that they are not an Infected Premises, Contact Premises, or Suspect Premises;
- *Free Premises (FP),* which are outside of a Control Area and not a Contact or Suspect Premises; or
- *Vaccinated Premises (VP),* where emergency vaccination has been performed. This may be a secondary premises designation.

Zones and Areas may surround premises, other zones, or locations where vaccination is taking place. These include:

- *an Infected Zone (IZ),* which surrounds *Infected Premises*;
- *a Buffer Zone (BZ),* which surrounds an Infected Zone or Contact Premises;
- *a Control Area (CA),* which includes the IZ and BZ;
- *a Surveillance Zone (SZ),* which surrounds the Control Area;
- *a Vaccination Zone (VZ),* which surrounds areas conducting vaccination; and
- *a Free Area*, which is an area not included in the CA.

The USDA has stated the minimum sizes of the zones/areas as well as the factors that should be used in determining that size. Examples of zones/areas and their minimum sizes are shown in Figure 2 and Table 1. Examples of the factors that help to determine the actual zone/area sizes include: jurisdictional areas, physical boundaries, premises' characteristics, environmental conditions, and premises biosecurity status (USDA, 2011).

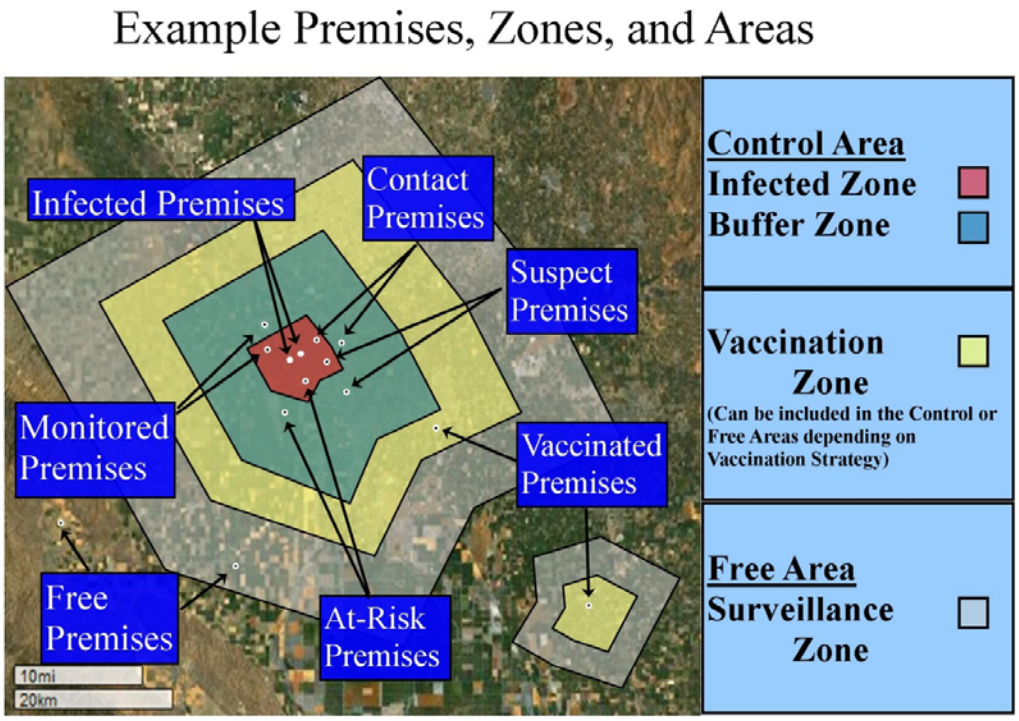

Figure 2. Examples of zones, areas, and premises (From USDA, 2011)

Table 1. Minimum sizes of zones and areas (From USDA, 2011)

Zone/Area	Minimum Size
Infected Zone (IZ)	At least 3 km beyond the perimeters of Infected Premises (IP)
Buffer Zone (BZ)	At least 7 km beyond the perimeter of IZ
Control Area (CA)	At least 10 km beyond the perimeter of the closest IP (sum of the IZ and BZ)
Surveillance Zone (SZ)	At least 10 km beyond the perimeter of the CA

The placement of zones and areas can have a major impact on the resource requirements needed to control an FMD outbreak. Large control areas have a higher certainty that all of the IPs are contained in the area and a lower probability that the virus will spread outside of the control area. However, they will also be more resource intense, have more premises to manage, and have a larger negative economic impact to normal business operations of uninfected premises in the zone. The opposite characteristics will be expected of smaller control areas (USDA, 2011).

D. LITERATURE REVIEW

FMD is well documented and has been reported in the literature since 1546 (Knowles, 1990). In light of this, we will focus this literature review on studies conducted to define disease-spread characteristics, studies that focus on an outbreak of FMD in California, and studies that use InterSpread Plus (ISP), the simulation software package we have chosen to use in our analysis of FMD spread.

The United States Animal Health Association's "Gray Book" (USAHA, 2008) provides a general overview of FMD, many of the disease-spread characteristics, as well as some of the strategies to control the spread. It is written for an audience of veterinarians and covers many foreign animal diseases. Mardones, Perez, Sanchez, Alkhamis, and Carpenter (2010) discuss the infectiousness durations for various susceptible species and attempt to parameterize them for use in simulation models. Sutmoller, Barteling, Olascoaga, and Sumption (2003) provide great detail on a number of topics covering FMD, including its epidemiology, vaccines, and control strategies. McLaws and Ribble (2007) study the relationship between outbreak size and early detection during outbreaks between 1992 and 2003, and find that there is no direct relationship. They attribute the movement of animals through markets as being the most critical factor in the size of an outbreak.

There have been several studies that simulate the spread of FMD in California, although most are limited to the Central Valley, where many of the large dairy facilities are located. Pineda-Krch, O'Brien, Thunes, and Carpenter (2010), however, conduct simulations of several areas of the state in places where reports of hunters killing feral hogs are high. Their results show that the duration and size of outbreaks are impacted greatly by where the outbreak occurred and on what type of facility, but they also find that a statewide movement ban decreases both of those measures consistently across location and type of facility infected. Bates, Thurmond, and Carpenter (2001) send surveys to livestock producers and others who would regularly visit livestock premises (e.g., veterinarians and hoof trimmers) in three central California counties in order to determine direct and indirect contact rates and movement distances in the study area. Direct contacts describe animal movement between two locations, while indirect contacts

describe the movement of humans, vehicles, equipment, or other mechanical means of spreading the virus between two locations. We use the results of this study extensively in this thesis to parameterize the network movement of the virus. Other California studies are by Kobayashi, Carpenter, Dickey, and Howitt (2007) and Carpenter, O'Brien, Hagerman, and McCarl (2011), which simulate the economic impact of an outbreak in California, and Carpenter, Christiansen, Dickey, Thunes, and Hullinger (2007), which determine the impact of an outbreak begun at the 2005 California State Fair.

For this thesis, we use ISP as the simulation software package for our experiments (Massey University, 2008). Initially developed for FMD at Massey University in New Zealand, ISP can be used to model any contagious disease and has been used extensively to model animal disease outbreaks before, during, and after they occurred in modern livestock countries including the United Kingdom, South Korea, and New Zealand. It is a "herd-based" model, where the unit spreading the disease is a farm or other livestock premises instead of an individual animal, and is stochastic, meaning that it includes randomness while modeling the disease spread.

The most prominent use of ISP was during the FMD outbreak in the U.K. in 2001. In writing about that outbreak, Keeling (2005) acknowledges the flexibility and modeling capability of ISP, but also states that it can be confusing and relies heavily on expert opinion for its parameterization. Yoon et al., (2006) utilize ISP to model alternative control strategies to those that were used during the 2002 outbreak of FMD in the Republic of Korea. They find that several proposed strategies could have reduced both the size and variability of the predicted number of infected farms. Dubé (2009) and Kostova-Vassilevska, Bates, Thurmond, and Carpenter (2004) provide descriptions of ISP in their studies of FMD models.

E. RESEARCH QUESTIONS

The main topic of this thesis will be to determine the best sizes of these areas and zones for the control of an FMD outbreak, while minimizing the negative impacts of those controls on the livestock industry in California. We decompose the main topic into

more specific questions in order to focus our research. We believe that by answering the following research questions, we can contribute to the body of knowledge of FMD spread and its control in California.

- Which disease spread parameters, such as the probability of disease transmission from a market or the rate at which animals are moved off of a large dairy farm, are most important to the simulation of an outbreak of FMD in California?
- In response to a variety of outbreak scenarios, what are the optimal sizes of Control Areas and Surveillance Zones that efficiently eradicate the disease and also minimize the economic impact on the livestock industry?
- How often should livestock facilities be screened for FMD prior to and during an outbreak?
- Which are the most dangerous outbreak scenarios modeled in this thesis for California?

This thesis makes several contributions from our research to the study and modeling of FMD in California.

- We undertake a significant data development effort to use a state-of-the-art animal disease simulation, ISP, to analyze potential FMD outbreaks in California. This data will also be available to future researchers.
- We develop an efficient design of experiment that allows us to simulate hundreds of thousands of possible FMD outbreaks in a relatively short amount of time. Then, we perform simulation analysis to identify key parameters affecting the spread and containment of an FMD outbreak.
- Finally, we develop and analyze eight specific outbreak scenarios relevant to FMD in California.

The ultimate objective is to provide insight into the effectiveness of various control strategies for application in policy decisions.

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II. METHODOLOGY AND DATA DEVELOPMENT

We use a simulation model and a designed experiment to evaluate robust governmental response strategies across a number of outbreak scenarios and a variety of disease parameters. We seek strategies that minimize the overall negative impact of the disease, whether that impact is caused by the disease itself or by the implemented disease control strategy. To that end, we divide this chapter into several sections. In Section A, we discuss the general usage of simulation to model FMD, some of the simulation software packages considered, and finally our choice of a software package. In Section B, we describe the dataset we received to input into the software, and how we interpret and modify this dataset to be able to input it into the software. In Section C, we describe the parameters used within the software to model the outbreak and its control, as well as the initial infection scenarios we developed. In Section D, we show the results of the initial plausibility testing of our model. Finally, in Section E, we describe the purpose and development of our experimental design and the measures we use to evaluate the effectiveness, robustness, and impact of various control strategies on the outbreak and the livestock industry in California. In our research, we use the term "farm" to describe the location where a group of animals is primarily housed and cared for on a permanent or semi permanent basis and "premises" to describe locations that could be farms or other livestock premises, such as markets or sales yards.

A. SIMULATION MODELLING OF FOOT AND MOUTH DISEASE (FMD)

1. Why Model?

Simulation modeling is used extensively to model FMD. Roger Morris (2008, slide 2) of Massey University lists the objectives of modeling a disease:

- To understand complex biological processes, and identify key features
- To test a biological hypothesis
- To predict the effect of interventions on occurrence of a disease
- To compare these predictions with reality after the event
- To guide difficult (e.g., nonrepeatable) management decisions

Our simulation will focus on the third and fifth of these as we seek to answer the research questions given in Chapter I, Section E.

2. Choosing a Simulation Software Package or Simulation Model

The choice of a model or software package to conduct the simulation is important because the use of a reputable software package enables us to have better confidence in the model's stability, verification, and validation, and thus the likelihood of producing a useful output. This is especially important when considering that we seek to inform policy decisions through the use of our model. In the next few paragraphs, we describe some of the current models and software packages used and our choice for the purposes of this project and its characteristics.

Several models are currently in use to simulate the outbreak of livestock disease. In addition to ISP, we also considered AusSpread (Garner & Beckett, 2005) and the North American Animal Disease Spread Model (NAADSM) (Harvey et al., 2007). Both are stochastic state transition models similar to ISP, but AusSpread is run using a Geographic Information System (GIS) called MapInfo. This allows the model output to be displayed on detailed maps. NAADSM is a stand-alone package that is easier to automate, but does not display the output information as well. Both are spatial in that they are able to model the proximity between livestock premises.

In 2005, AusSpread, ISP, and NAADSM were compared at a workshop on FMD modeling and policy development by the Quadrilateral (QUADS) countries (Australia, Canada, New Zealand, and the United States). The QUADS compared the results of these models, using several FMD scenarios. Even though AusSpread and ISP are able to explicitly model the network spread of FMD, while NAADSM is not—although there are methods within that model to at least partially account for network spread (Dubé, 2009)—the results were similar. Although there were statistically significant differences between the outputs of the three models for a given outbreak scenario, the researchers in attendance believed that any decisions based on the output of each model would not have differed (Dubé et al., 2007). Ultimately, we chose to use ISP because it

is a well-known and well-used software package that is able to model the spatial, temporal, and network spread of FMD, and is easily automated to run on multiple networked computers. The latter is important to the use of an experimental design.

3. Characteristics of the Chosen Model

ISP is a stochastic, state-transition model where the premises are in one of several states at any time. Examples of these states are: susceptible to infection, infected with the disease, or immune to the disease. The software user is also allowed to define additional states within the model, such as whether the premises are in a control area or a vaccination zone. Premises may be in multiple states at one time (see Figure 3). There are constraints on the allowable transitions from one state to another. For example, in order for premises to move from "in Vaccination Zone" to "Vaccinated," a "Vaccination Resource" must be available to vaccinate the premises. Having an available Vaccination Resource would be called a "trigger" for this state transition. A table with a mapping of all of the state transitions used in this model and their triggers is included in Table 2. ISP separately represents many transmission processes, disease characteristics, and control methods in both space and time. All of these processes and characteristics help determine what state premises are in at a particular point in time. We provide details of these processes in Section C and an overview in Figure 4.

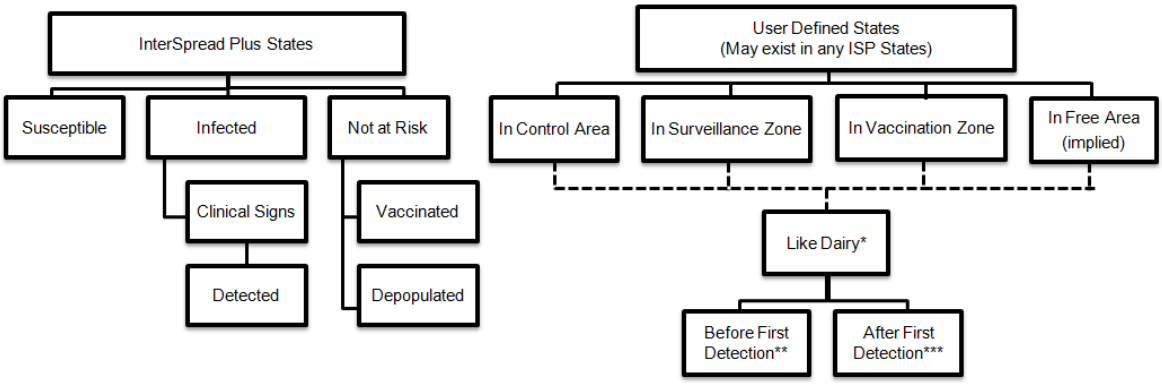

Figure 3. States used in the model

Table 2. The state trigger matrix. This matrix shows which triggers allow premises to move into a new state. Depending on the states involved, the new state may be in addition to or a replacement of the original state. For example, the only way that a farm can move into the state "In Control Area" is by an infected premises being detected within the control area, outside the radius distance from the farm. In this example, the farm described would retain the state "Infected" and have an additional state of "In Control Area."

State Trigger Matrix

Current State	New State: Infected	Susceptible	Infected / Clinical Signs	Infected / Clinical Signs / Detected	Not at Risk / Depopulated	Not at Risk / Vaccinated	In Control Area	In Surveillance Zone	In Vaccination Zone	Like Dairy	Like Dairy: Before First Detection	Like Dairy: After First Detection
None (Sim Start)	1	2	X	X	X	X	X	X	X	3	3	X
Infected	-----	X	6	X	X	X	8	9	10	S	S	S
Infected / Clinical Signs	-----	X	-----	7	X	X	8	9	10	S	S	S
Infected / Clinical Signs / Detected	-----	X	X	-----	11	X	8, 13	X	X	S	S	S
Susceptible	4, 5	-----	X	X	X	X	8	9	10	S	S	S
Not at Risk / Depopulated	X	X	X	X	-----	X	X	X	X	S	S	S
Not at Risk / Vaccinated	X	X	X	X	X	-----	8	9	S	S	S	S
In Control Area	S	S	S	S	S	S	-----	X	10	S	S	S
In Surveillance Zone	S	S	S	S	S	S	8	-----	10	S	S	S
In Vaccination Zone	S	S	S	S	S	12	8	S	-----	S	S	S
Like Dairy	S	S	S	S	S	S	S	S	S	-----	S	S
Like Dairy: Before First Detection	S	S	S	S	S	S	S	S	S	S	-----	14
Like Dairy: After First Detection	S	S	S	S	S	S	S	S	S	S	X	-----

Trigger	Code
Same State/Substate	-----
No Trigger Allows this Change	X
Simultaneous States Allowed	S
In Epidemic History File	1
Not in Epidemic History File	2
Premise Type:	3
Movement Transmission	4
Local Spread Transmission	5
Time Until Clinical Signs Complete	6
Surveillance Successful	7
Infected Premise Detected Within the Control Area Outside Radius distance from this premise.	8
Infected Premise Detected Within the Surveillance Zone Outside Radius distance from this premise.	9
Infected Premise Detected Within the Vaccination Zone Outside Radius distance from this premise.	10
Depopulation Resources are available	11
Vaccination Resources are available	12
Depopulation Resources are not available	13
First Premise Detected during this Iteration.	14

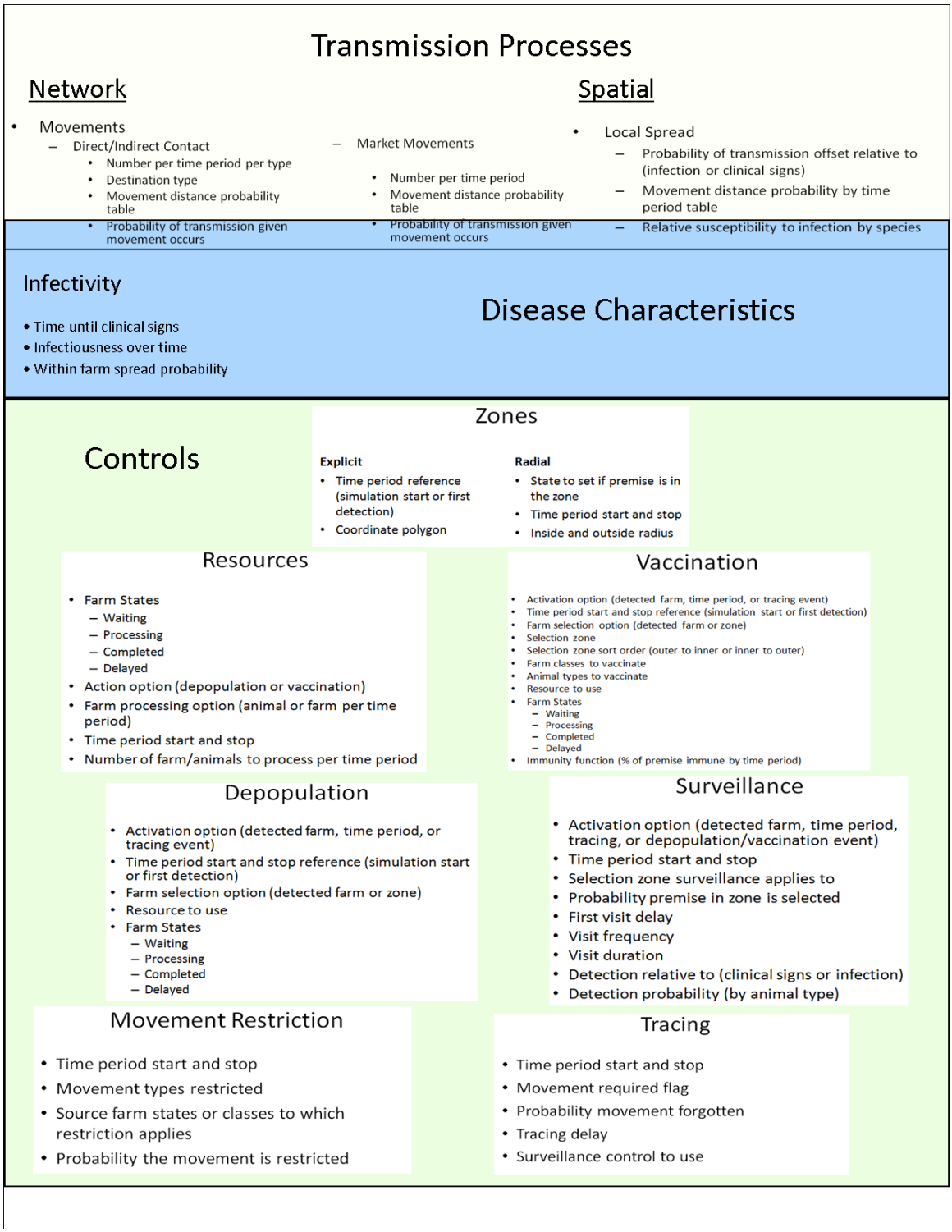

Figure 4. The transmission processes, disease characteristics, and control methods used in our simulation. Notice that some overlap exists between "Transmission Processes" and "Disease Characteristics." Some parameters listed under "Movements" are actually characteristics of the disease.

B. DATA DESCRIPTION

In this section, we describe the inputs required by the ISP software. Specifically, we describe the dataset acquired for use in our modeling and our procedure to interpret and modify it for use by ISP.

1. Description of the Dataset

Although CDFA maintains careful statistics on the location and sizes of individual farms in California, such information is proprietary and not available to the public for modeling or analysis. The dataset we use in this thesis is described in Melius, Robertson, and Hullinger (2006) and includes 25,655 premises locations organized into the seven columns described below. A sample from the original data is shown in Table 3. The data were developed from publicly available, county-level, aggregated statistics of livestock premises provided by the National Agricultural Statistics Service (NASS) (NASS, 2010). As such, they are an approximation of the locations, sizes, animal types, and production types of the livestock premises in the state of California. The location coordinates shown are heterogeneous random locations, selected based on a weighting scheme using the altitude, flatness, human population, and land use of an area. The size of the premises is selected by uniformly varying the size according to premises type so that the average size of each premises type is preserved for each county (Hullinger, 2012). We interpreted the original data as described below:

- *Premises*: a concatenation of the premises type name and the unique identifier for each premise.
- *ID*: an integer representing a unique identifier for each premise (same integer as the unique identifier in "Premises").
- *Type*: a numeric code for the type of premises. Included in the data were 26 of these codes. Premises populated with cattle are assigned codes between 1 and 99; those populated with swine are assigned codes between 100 and 199; those populated with sheep are assigned codes between 200 and 299; and those populated with goats are assigned codes between 300 and 399. Additionally, code 511 indicates a cattle market and code

512 indicates a swine market. We give a complete listing of the type of codes used in the original data in Table 4.

- *Size*: an integer designating the number of animals on the premises. We assume that only one type of animal is on each of the premises.
- *FIPS*: the Federal Information Processing Standard (FIPS) code for the state and county in which the premise is located.
- *Lat*: Latitude of the centroid of the randomized premise location.
- *Long*: Longitude of the centroid of the randomized premise location.

Table 3. A sample of the original data provided by Lawrence Livermore National Laboratory (LLNL)

Premises	ID	Type	Size	FIPS	Lat	Long
Dairy(L):0	0	33	940	6115	39.01372910	-121.5098953
Dairy(L):1	1	33	1,379	6115	39.29288864	-121.5932312
Dairy(L):2	2	33	1,819	6115	39.17738724	-121.4760590
Dairy(L):3	3	33	2,258	6115	39.26313400	-121.5667267
Stocker(S): 4	4	61	12	6115	39.10063934	-121.4598846
Stocker(S): 5	5	61	15	6115	39.29784775	-121.5664749

Table 4. Descriptive Statistics of the Data by Premises Type. Premises column includes the following codes: B-Backyard, S-Small, M-Medium, L-Large. A description of the development of this dataset is found in NASS (2012).

Premises	Species	Type Code	Total Animals of Type	No. of Premises	Min No. Animals	Max No. Animals	Avg No. Animals	StdDev of Size
Beef(B)	cattle	24	44,396	5,673	1	10	7.826	1.39
Dairy(S)	cattle	31	7,243	103	13	174	70.320	43.35
Dairy(M)	cattle	32	26,900	103	202	495	261.165	58.87
Dairy(L)	cattle	33	2,649,565	1,526	506	7,458	1,736.281	1,057.47
Dairy(B)	cattle	34	1,518	433	1	9	3.506	1.85
CowCalf(S)	cattle	41	458,635	4,877	10	473	94.040	61.83
CowCalf(L)	cattle	43	423,605	237	521	75,512	1,787.363	5,424.75
Feedlot(S)	cattle	51	7,965	95	11	381	83.842	81.28
Feedlot(L)	cattle	53	563,073	30	1,102	49,667	18,769.100	17,135.79
Stocker(S)	cattle	61	199,791	1,952	11	496	102.352	89.49
Stocker(L)	cattle	63	175,339	139	212	18,933	1,261.432	2,058.68
DCalfRanch(L)	cattle	73	576,634	44	1,314	34,276	13,105.318	9,070.17
Swine(B)	swine	114	5,287	1,203	1	16	4.395	2.33
SwineFWean(S)	swine	121	1,653	15	37	426	110.200	100.37
SwineFinish(S)	swine	131	4,904	49	31	507	100.082	92.08
SwineFFeeder(S)	swine	151	2,267	24	31	426	94.458	84.84
SwineFFeeder(L)	swine	153	23,840	2	11,920	11,920	11,920.000	N/A
SwineFarFin(S)	swine	161	8,371	87	29	552	96.218	94.19
SwineFarFin(L)	swine	163	107,280	9	8,280	15,560	11,920.000	2,573.87
Sheep(S)	sheep	211	94,524	1,092	26	375	86.560	51.07
Sheep(L)	sheep	213	474,764	78	1,365	33,178	6,086.718	4,639.32
Sheep(B)	sheep	214	26,088	2,893	1	23	9.018	4.87
Goats	goat	310	104,596	2,296	18	244	45.556	31.17
Goats(B)	goat	314	26,175	2,689	1	19	9.734	5.07
Market(Cattle)	cattle	511	2250	15	150	150	150	N/A
Market(Swine)	swine	512	100	1	100	100	100	N/A
Grand Total			**6,016,763**	**25,665**	**1**	**75,512**	**234.435**	**1,394.04**

2. Our Procedure to Interpret and Modify the Dataset for Use in ISP

Each run of an ISP model requires several inputs. These take the form of text files and include:

- a "Farm File" that describes the premises in the study area;
- a "Contact Location" File that describes the markets and other gathering places of animals from multiple locations;
- an "Epidemic History File" that lists the premises which are in the "infected" and/or "detected" states at the beginning of the simulation; and

- a "Zone File" listing the boundaries of the area of study in the form of a series of coordinates forming a polygon.

We describe these inputs in more detail in the following paragraphs.

a. The Farm File

This file is essential to ISP because it describes in detail the area to be simulated. At a minimum, it must include:

- Cartesian coordinates defining where susceptible animals are located (can be in the form of a centroid or polygon, but here we use the centroid of the premises);
- the number of animals located at each of the premises;
- and a premises type for each location (e.g., large dairy, small cattle feedlot, backyard swine premises).

An arbitrary number of additional columns of user-defined data can also be included in the farm file to further describe the modeling environment. Next, we describe the development of our farm file.

In order to develop this farm file, we create a computer program, or "script," written in the R Programming Language (R Development Core Team, 2012) to manipulate the data from the format described above to a text file for import into ISP. Our first task is to transform the latitude/longitude coordinates provided in our dataset to integer Cartesian coordinates, as required by ISP. We first add a "zone" column to each of the premises in the farm file and populate it with an integer between 1 and 6, which corresponds to the correct California Coordinate System (CCS83) zone to use when transforming the latitude/longitude columns to northerly/easterly coordinates. The units of the CCS83 coordinate systems are meters. The correct zone is found by mapping the FIPS code to the CCS83 zone listed in California Department of Transportation (Caltrans) (1993). We then use R script, which incorporates the R package "rgdal" (Stevenson, 2012) as a template to transform the data from latitude/longitude to northerly/easterly coordinates. We are unable to use the correct zone for each FIPS code while keeping the correct spatial relationship between the zones. So, we use Zone 3 as

the projection for all of the premises locations. From our initial analysis of the distortion this causes between premises in the far north and far south of the state, it appears that the incorrect zone usage will not adversely affect our analysis of the simulation.

Next, we split the "Size" column to show the number of each animal species on each premises. We add five additional columns to indicate species (cattle, swine, sheep, goat, and other) and initially populate them with zeros. We develop a mapping table between the "type" column and a "species" column based on the type described by the "Premises" column in the original data, and use an R script to copy the number in the "Size" column to the appropriate species column.

Finally, we create another R script to determine the distance between each of the premises and all other premises in the dataset. This allows us to add six columns to the data to describe the density of premises and animals within a 3-, 10-, and 20-kilometer (km) radii from each of the premises in the dataset. We will use these columns to help determine the impact of premises density and animal density on how the disease spreads within California. These computations are subject to the fact that the locations given in the dataset are generated by an algorithm and are not the actual locations of premises. However, we assume that the generated data is representative of the true locations enough to use these densities in our analysis. We show the distributions of the densities of premises and animals within the state in Figure 5. We show similar information in Figures 6 and 7, but display it so that the reader can visualize where the densely populated areas are located in California. We then show a sample of the farm file in its final form in Table 5 and describe its columns below.

- *id*: unique identifier (same as original data)
- *type*: numerical code for premises type (same as original data)
- *FIPS*: the FIPS code for the state and county in which the premises are located (same as original data)
- *cattle*: number of cattle on the premises
- *swine*: number of swine on the premises
- *sheep*: number of sheep on the premises
- *goat*: number of goats on the premises

- *other*: number of other animals on the premises (all zeros for this dataset)
- *premises*: description of the type of premises. We develop this column from the "Premises" column in the original dataset. After splitting the original column into two columns, a string representing the premises type name and an integer representing the unique identifier, we remove the unique identifier column because it is a duplicate of "id."
- *premises_3k*: number of other premises within a 3-km radius of the given premises
- *animal_3k*: number of animals (all species) within a 3-km radius of the given premises
- *premises_10k*: number of other premises within a 3-km radius of the given premises
- *animal_10k*: number of animals (all species) within a 3-km radius of the given premises
- *premises_20k*: number of other premises within a 3-km radius of the given premises
- *animal_20k*: number of animals (all species) within a 3-km radius of the given premises
- *xcoord*: easterly coordinate (transformed from longitude using a CCS83 Zone 3 projection)
- *ycoord*: northerly coordinate (transformed from latitude using a CCS83 Zone 3 projection)

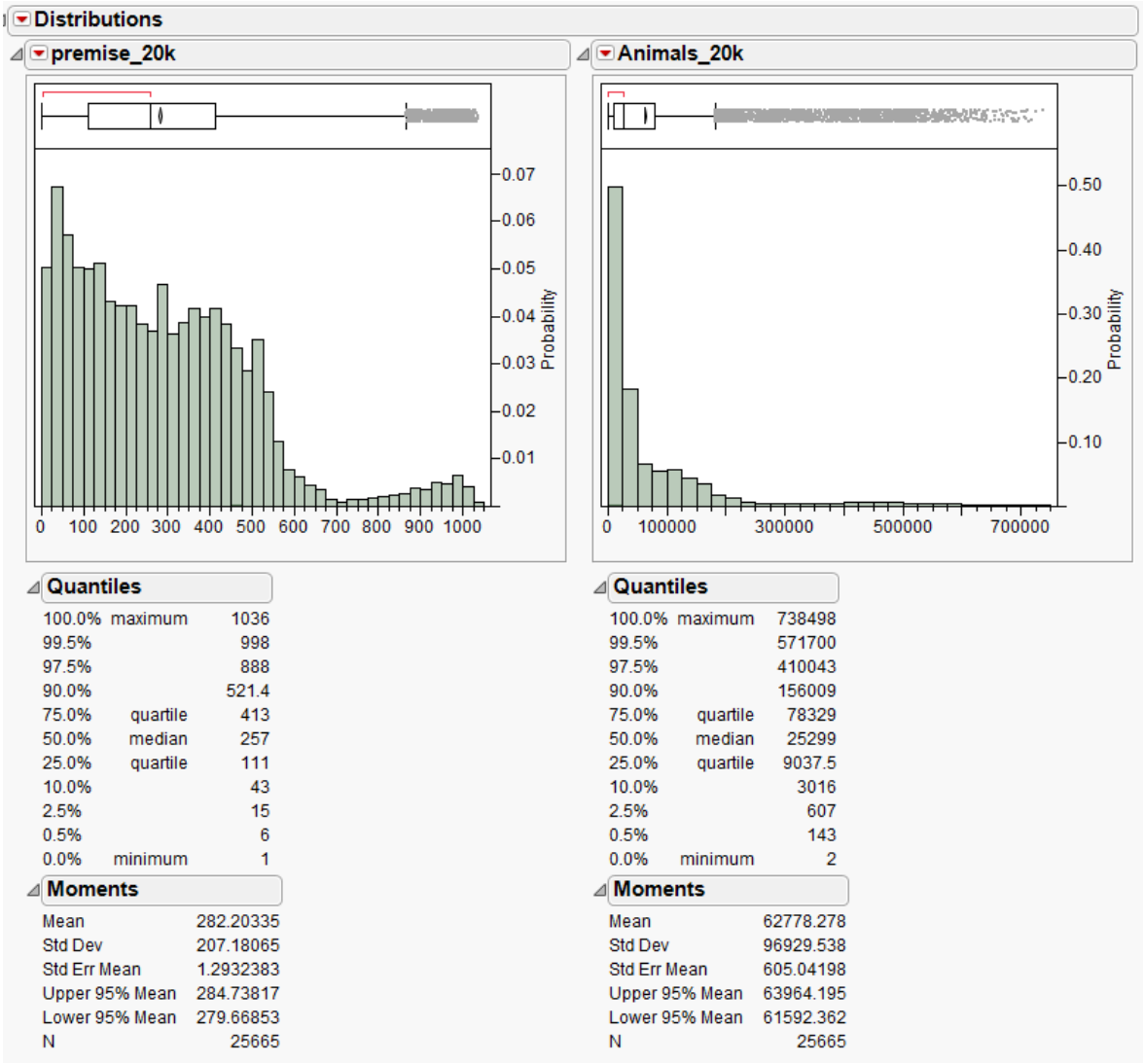

Figure 5. Histograms and descriptive statistics of the within 20-km densities of premises and animals. The histograms show the proportion of premises (y-axis) that have premises or animal densities of the amount shown along the x-axis. One interesting comparison between these two densities is how differently they are shaped. Premises densities are much more uniformly distributed between densities of 0 and 525 premises and the distribution is bimodal. Animal densities, however, are highly skewed, with almost 50% of the premises having densities of less than 25,000 animals.

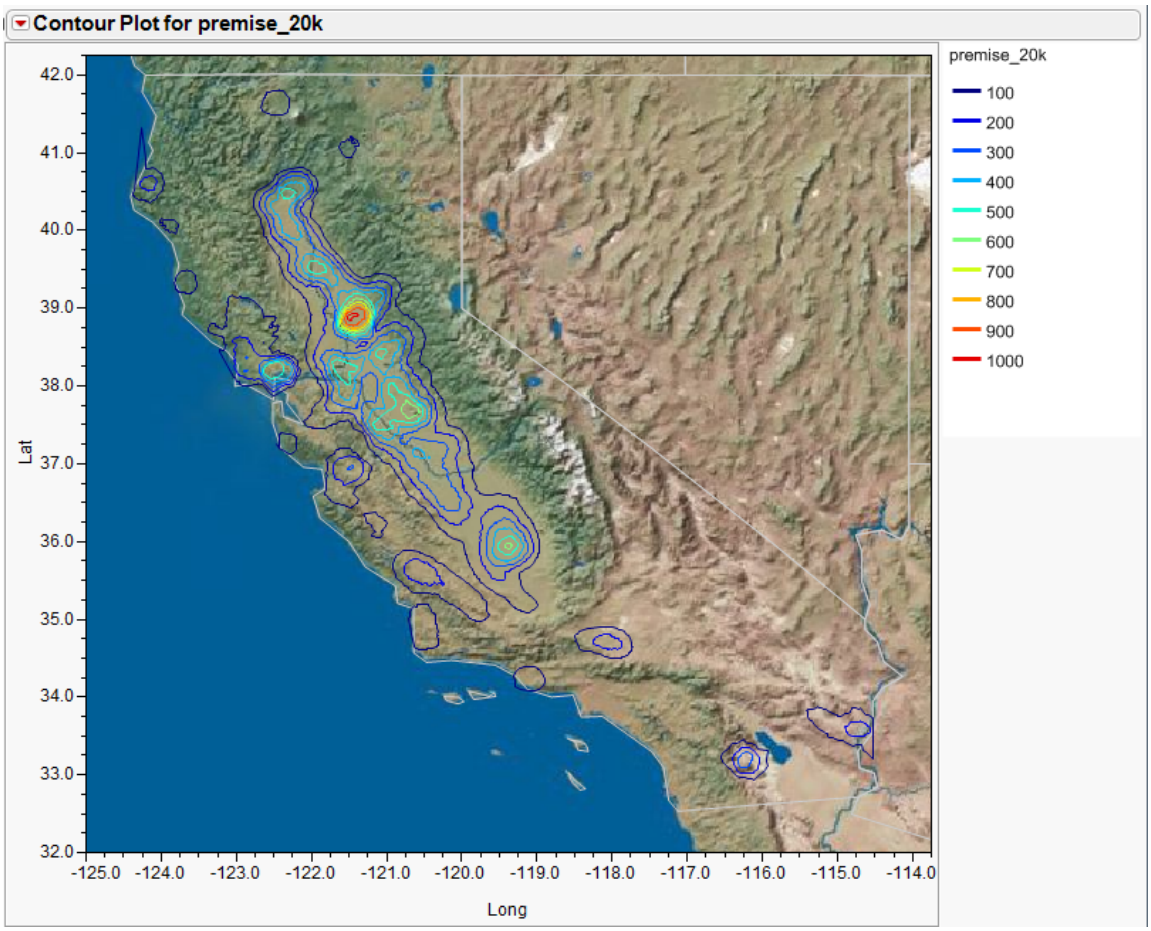

Figure 6. Contour plot showing the density of premises within 20 km of each premise in the dataset. Contour lines indicate that premises within the contour have a 20-km premise density of at least the amount indicated in the legend.

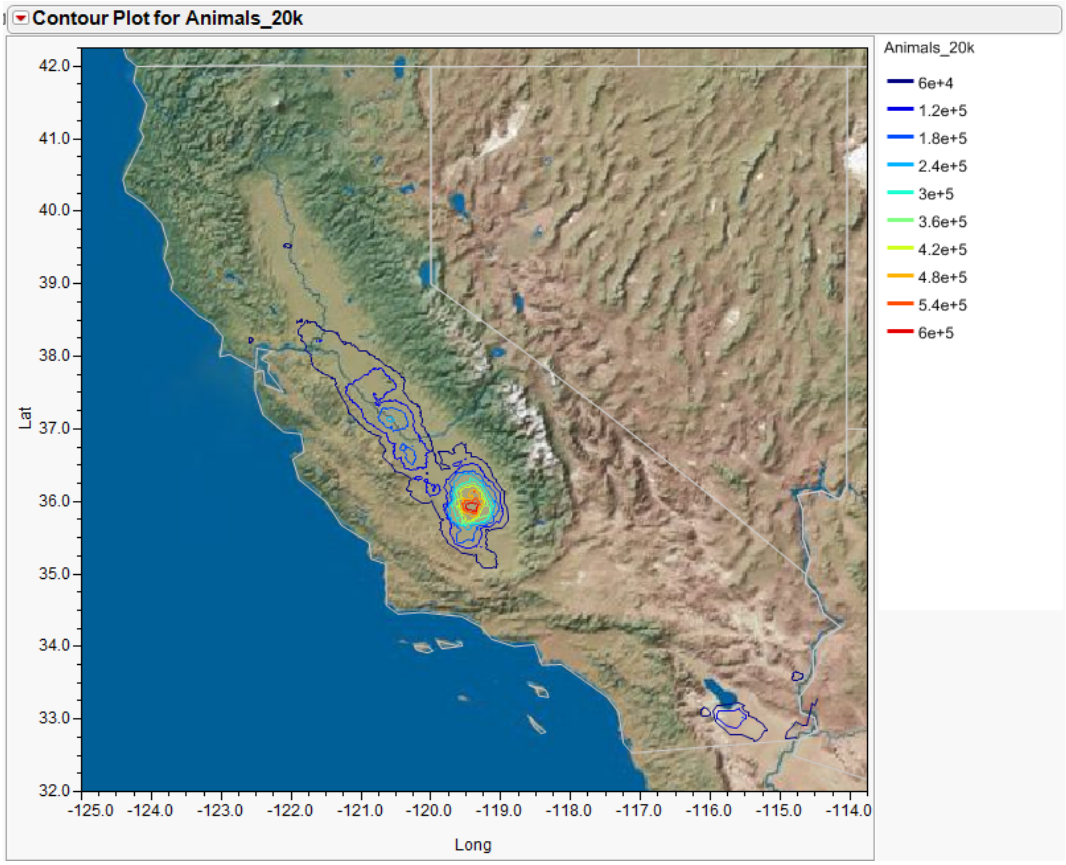

Figure 7. Contour plot showing the density of animals within 20 km of each of the premises in the dataset. Contrast the location of the animal densities in this plot with the premises densities in Figure 6 and notice how the most premises-dense areas do not necessarily correspond to the most animal-dense areas. For example, areas in Northern California are premises dense, but are not animal dense.

Table 5. Example of the farm file loaded as input into ISP

ID	Type	FIPS	Zone	cattle	swine	sheep	goat	other	Premise	premise_3k	premise_10k	premise_20k	animal_3k	animal_10k	animal_20k	xcoord	ycoord
0	33	6115	2	940	0	0	0	0	Dairy(L)	16	143	705	1192	3948	23866	1912519.926	779478.177471014;;
1	33	6115	2	1,379	0	0	0	0	Dairy(L)	33	175	387	2289	9363	16617	1905663.556	810556.164516908;;
2	33	6115	2	1,819	0	0	0	0	Dairy(L)	18	167	467	2243	6213	19549	1915640.347	797618.708362427;;
3	33	6115	2	2,258	0	0	0	0	Dairy(L)	35	205	396	3778	10141	17044	1907912.902	807225.65922504;;
4	61	6115	2	12	0	0	0	0	Stocker(S)	25	158	594	606	5444	18911	1916950.823	789082.385581495;;
5	61	6115	2	15	0	0	0	0	Stocker(S)	36	182	380	2290	9576	16439	1907978.569	811080.21527166;;

b. The Contact Location File

We create another R script to generate a text file to describe the locations of cattle and swine markets. These are subsets of the farm file where “type” equals “511”

for cattle and "512" for swine. We then delete the columns not required by ISP; leaving only the coordinates for the market locations (see Table 6).

Table 6. Example from the contact location file ("market file") loaded as input into ISP

x.coord	y.coord
2011429.535	580151.1126
2448099.754	273631.5867
1871501.834	848398.2476
1941376.126	702667.1927
2089696.962	354119.2982
1926198.788	1037604.677
2080077.613	472644.6281
2408090.623	418024.6536
2057510.191	360616.3969
1840739.37	935907.2295
1706699.847	902676.6741
1711862.379	1037000.539
2535829.592	323243.2416
1975990.614	640885.5455
1976822.924	617930.786
2087141.126	495456.172

c. The Epidemic History File

This file describes specifically which premises are currently infected and if they are detected. If the infected premises are not currently detected, it will also state on which day the infected premises are detected. During initial plausibility testing of the model, we include one randomly selected cattle premise from Central California without a time until detection in this file. This premise is a Cow/Calf operation, with 168 cattle in a high premises-dense area near Redding, California.

d. The Zone File

In order to show a rough estimate of the area of analysis, California, we construct a polygon shape file by using Google Maps to find latitude/longitude coordinates for a rough outline of California. We then use an R script to transform these

into CCS83 coordinates that can be used by ISP. Zone 3 is used to transform all coordinate pairs of the polygon. Figure 8 shows all of the coordinate data included in all of the ISP input files combined on a single plot.

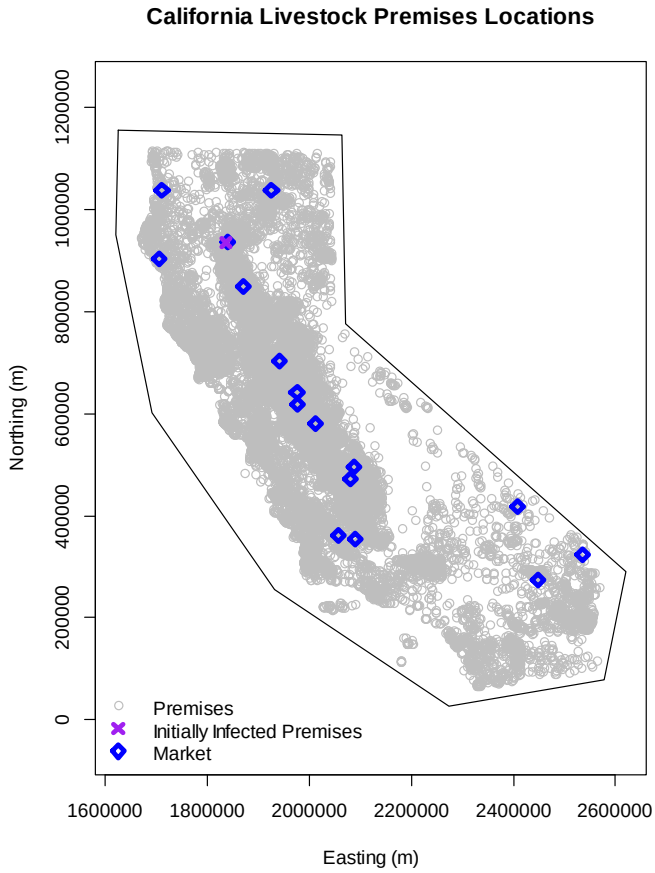

Figure 8. California Premises Locations: Shown are the locations of all coordinate data input into ISP for the initial plausibility testing of the model.

C. SIMULATION SOFTWARE PARAMETER AND INITIAL INFECTION SCENARIO DEVELOPMENT

Our first task is to determine a plausible model for how the disease could spread through California without any controls. This is not to say that this model is predictive of an actual outbreak of the disease, but that it is plausibly representative of how an

outbreak could spread. Then, we develop a model using a generic control strategy and the same disease spread parameter settings as the uncontrolled model's settings. In Chapter III, we describe and compare the results of this plausibility testing.

In order to accomplish the development of these two models, we assembled a team at the International Data Farming Workshop held March 25–30, 2012, at the Naval Postgraduate School in Monterey, California to study the problem. The team included several experts in simulation modeling, computer science, and two veterinarians who are currently students of the School of Veterinary Medicine at the University of California, Davis and are studying to attain a Master of Preventive Veterinary Medicine (MPVM) degree. This team helped us determine the sets of parameters for both the spread of the disease as well as many of the control parameters shown in Section 4. We divide the section into six subsections:

- **Overview of the Control File**, which briefly describes the text file used to input parameter settings into ISP. The control file contains one row pertaining to each parameter described in the next three topics.
- **Development of the Model Parameters**, which describes the parameters affecting how the model is run. These include such things as the random number generator to use and the number of iterations to run the simulation.
- **Development of the Disease Spread Parameters**, which describes the network and spatial parameters affecting how the disease is spread from premises to premises during the simulation.
- **Development of the Disease Spread Control Parameters**, which describes the strategies and policies to control the spread of the disease as well as the constraints to those strategies and policies.
- **Development of Starting Scenarios**, which describes the initially infected premises for eight different scenarios that we model.

1. Overview of the Control File

ISP is designed to operate from the command line of a Linux- or Windows-based single computer, or multiple networked computers, with only one argument specifying the control file to be used by the software to simulate disease spread. The *control file* describes to ISP how the model, disease, and control parameters are used to simulate the spread of a herd-based disease, both temporally and spatially, through a population. The development of the control file can be accomplished through the use of a text editor, by a scripting software language, or by the Control File Editor graphic user interface, which is packaged with the Windows version of ISP. This text file method enables the modeler to automate the model to make many different runs of a simulation using many different scenarios or include different farm, market, or epidemic history files, depending on the focus of the analysis. We show a sample control file in Appendix B.

2. Development of the Model Parameters

The model parameters section of the control file describes to ISP some basic information about how the model should be run. In our model, we include the number of iterations to be completed during the run, the number of time periods to model, a specific random number generator and seed to use during the run, the maximum infected premises allowed during the iteration, and a set of user-defined farm states. The parameter settings and the rationale we use to develop them are given below.

- *Iteration Count*: 100. This is a medium-sized number of runs chosen to satisfy our computational limitations. The statistical significance from the experiments is discussed in Chapter V.
- *Time Period Count*: We use 100 days during the experimental design and 40 days during our initial testing. Similar to the iteration count, we consider 100 days as a medium-sized number that gives us a good idea of disease behavior without overtaxing processing capability.
- *Seed*: Randomly chosen using a Mersenne Twister generator (Matsumoto & Nishimura, 1998).

- *Random Generator Name*: TRandomMotherOfAll, which is a low-resolution, low-speed generator with low memory usage (Stevenson, 2012).
- *Max Infected Farms*: 7,700, which is 30% of the total number of premises in our dataset. We set this limit because we feel that if 30% of premises in California are infected, the control measures used at the beginning of the outbreak will be considered ineffective and be replaced with a new strategy.
- *User-Defined Farm States*
    - *In Control Area*: Premises have been placed in the Control Area. We trigger this state either when the premises are infected and detected, or when another premise located at a distance less than or equal to the designated Control Area outside radius has been detected.
    - *In Surveillance Zone*: Premises have been placed in the Surveillance Zone. We trigger this state when another premise located at a distance less than or equal to the designated Surveillance Zone outside radius has been detected.
    - *In Vaccination Zone*: Premises have been placed in the Vaccination Zone. We trigger this state when another premise located at a distance less than or equal to the designated Vaccination Zone outside radius has been detected.
    - *Waiting for Vaccination*: The premises have been placed in the Vaccination Zone and are awaiting resources to become available to begin vaccination of the animals on the premises.
    - *Processing Vaccination*: Resources have begun vaccination of the animals on the premises, but are not yet finished with the process.
    - *Vaccinated*: All animals on the premises have been vaccinated.

- *Waiting for Depopulation*: The premises have been infected, detected, and are awaiting resources to become available to begin depopulation of the animals on the premises.
- *Processing Depopulation*: Resources have begun depopulation of the animals on the premises, but are not yet finished with the process.
- *Depopulated*: All animals on the premises have been depopulated.
- *likeDairy*: Premises have similar surveillance practices to a dairy facility. These include premises designated as: Dairies (Small-S, Medium-M, Large-L), Feedlots (S, L), and Dairy Calf Ranches.
- *likeDairy before first detection*: Premises are designated as "likeDairy" and no premises have been detected during the current iteration.
- *likeDairy after first detection*: Premises are designated as "likeDairy" and at least one of the premises has been detected during the current iteration.
- Additional states that were defined, but not used, during this experiment were *Delayed Vaccinated* and *Delayed Depopulated.*

The SetState section of the control file allows the ISP user to designate some types of premises to a certain modeling state at the beginning of the simulation. We used this section to designate a modeling state of likeDairy to all Dairy (S, M, L), Feedlot (S, L), and Dairy Calf Ranches, and we use this modeling state to specify certain surveillance parameters to use just for dairy and dairy-like premises during the simulation.

3. Development of the Disease-Spread Parameters

ISP has the ability to model many different disease-spread parameters, which describe the network and spatial disease spread from premises to premises during the simulation. The sections in the control file describing these parameters are titled: *movement type, route, fixed route, local spread, airborne spread, and infectivity.* Of these, we do not use route and fixed route, which model specific routes between premises

(e.g., a milk truck pickup route between several dairy facilities), because data at this level of detail is not currently available through public sources for California. We also do not use the airborne spread parameter within ISP. Instead, we assume that varying the local spread distance parameter will account for the majority of the aerosol spread of the disease. This assumption is reasonable given that we are modeling a broad range of local spread distances and the fact that some types/subtypes of the FMD virus do not spread long distances by aerosol. Additionally, serotype O, which has been responsible for many recent outbreaks in temperate countries, has shown little tendency for airborne spread (Stevenson, 2012). We subdivide this section of the thesis by describing the following sections in the control file:

- **Movement Type:** Network spread of the disease
- **Local Spread:** Spatial spread of the disease over time
- **Infectivity:** Disease characteristics affecting disease spread

a. Movement Type

Even though the zones/areas discussed in Chapter I and Figure 2 seem to be purely spatial in design, the USDA has recognized that the network spread of FMD should be considered when designating these zones/areas and recommends the use of these types of factors in those determinations. Since the virus is easily spread in many ways, direct and indirect contacts between livestock facilities could happen over greater distances than are accounted for in a purely spatial design. Direct contact at highly connected operations, such as livestock markets, occupy a central role in the flow of animals and should be dealt with differently than other premises in an outbreak area (Dubé, 2009). Indirect contact, such as by artificial insemination teams or hoof trimmers, may be higher at different types of operations than others. In a survey of livestock facilities in California, for example, large swine operations had an over 3,600% higher mean reported monthly indirect contact rate than small beef farms (Bates et al., 2001). This seems to be a function of both the size of the herd as well as the species at the facility.

In order to account for the network spread of the disease, ISP uses movement types to model direct and indirect contact between animals. For our analysis, we model 18 movement types. The first 11 describe individual farm-to-farm movements, the next two model farm-to-market and market-to-farm movements, and the last five model indirect farm-to-farm movements.

For each of these movement types, we developed the movement distances and corresponding probabilities using empirical distributions described by Bates et al. (2001), in which the authors study central California direct and indirect livestock contact rates and movement distances. We choose to model all direct and indirect movement frequencies within our model, with Poisson distributions with parameters, as shown in Table 7. We estimate the probability of each direct contact movement type to reach different distance bands by using the data shown in several graphs in Bates et al. (2001) and show those probabilities in Table 8. The probability of transmission of FMD among different species is a poorly understood parameter and is not easily defined across serotypes and subtypes of the disease. Orsel, Bouma, Dekker, Stegeman, and De Jong (2009) study the virus transmission of piglets, lambs, and calves, and compare them to each other. After analyzing their study, we set the probability of transmission given a farm-to-farm movement occurs to be a function of the species of animal located on the premises where the movement began. The probability of transmission for sheep and goats are set to a constant probability, p. For determining a plausible uncontrolled spread, p = 0.2. We set the probabilities for cattle and pigs to $1-(1-p)^{1.82}$ and $1-(1-p)^{80}$, respectively. This equates to saying that a pig is about 80 times more infectious than a sheep or goat.

Table 7. Shipments from livestock premises. We consider the numeric premises "Type Codes" from our data to be equivalent to the "Facility Types" from Bates et al. (2001). Green highlighted columns in this table show the data or calculations we add to the authors' data. The "Actual Mean" column is calculated by multiplying the "Mean Shipments" by the "% reporting shipments." The "Average Daily Shipments λ" is the "Actual Mean" column divided by 30 to determine a daily rate. This column was used in determining the plausibility of the model. The similarly calculated "Average Daily Shipments +/– 95% CI" columns are used as high and low limits within the experimental design for their corresponding movement type rates.

Shipments from the Livestock Premise											
Type Codes	Premise Type	No. Responding	No. Reporting Shipments	Reporting Shipments	Mean Shipments (Monthly)	-95%CI	+95%CI	Actual Mean	Avg. Daily Shipments λ	Avg. Daily Shipments -95%CI	Avg. Daily Shipments +95%CI
24, 34, 114, 214, 314	Backyard	31	29	93.55%	1.7	0	4.2	1.590	0.053	0.000	0.140
310	Goat	3	3	100.00%	6.6	0	16.8	6.600	0.220	0.000	0.560
211, 213	Sheep	15	15	100.00%	7.9	0	18.8	7.900	0.263	0.000	0.627
	Beef										
51, 61	< 250	52	52	100.00%	0.9	0.5	1.3	0.900	0.030	0.017	0.043
53, 63	>= 250	29	28	96.55%	2	0	3	1.931	0.064	0.000	0.100
	Dairy										
31, 32	< 1000	54	52	96.30%	8.2	4.3	12.1	7.896	0.263	0.143	0.403
none	1000 - 1999	54	54	100.00%	17.4	12.5	22.3	17.400	0.580	0.417	0.743
33	>= 2000	48	48	100.00%	16.4	11.9	20.9	16.400	0.547	0.397	0.697
	Calf/heifer										
41	< 250	10	10	100.00%	0.7	0.3	1.1	0.700	0.023	0.010	0.037
43, 73	>= 250	4	4	100.00%	22.4	0	58.8	22.400	0.747	0.000	1.960
	Swine										
121, 131, 151, 161	< 2000	12	11	91.67%	4.8	1.1	8.5	4.400	0.147	0.037	0.283
153, 163	>= 2000	5	5	100.00%	20	0.2	39.8	20.000	0.667	0.007	1.327
t =	30										

Table 8. Movement Distance Probabilities used to model farm-to-farm movements. We estimate the probabilities from the corresponding graphs in Bates et al. (2001). Again, we consider the numeric premises "Type Codes" from our data to be equivalent to the "Facility Types" from Bates et al. (2001).

Average Probability for Specified Distance Travelled To/From a Livestock Premise (Distance in Meters)										
Type Code	Facility type	19,000	39,000	59,000	79,000	99,000	119,000	139,000	159,000	179,000
24, 34, 114, 214, 314	Backyard	0.615	0.110	0.025	0.060	0.010	0.035	0.010	0.000	0.135
211, 213, 310	Goat/Sheep	0.365	0.160	0.090	0.035	0.010	0.000	0.015	0.025	0.300
51, 53, 61, 63	Beef	0.390	0.220	0.125	0.055	0.025	0.010	0.020	0.015	0.140
31, 32, 33	Dairy	0.570	0.255	0.035	0.010	0.005	0.010	0.005	0.005	0.105
41, 43, 73	Calf/heifer	0.410	0.145	0.205	0.000	0.000	0.000	0.020	0.000	0.220
121, 131, 151, 153, 161, 163	Swine	0.315	0.290	0.020	0.050	0.120	0.045	0.015	0.000	0.145

We continue to use Bates et al. (2001) as a basis to develop the parameters for indirect contact movements. We calculate monthly indirect contact movement rates by subtracting the employee and friend columns from the total mean number of monthly indirect contacts shown in the authors' data, in order to model only higher risk, indirect contact. We assume employees and friends are lower risk due to their limited exposure to

animals on other livestock premises on a single day; however, this may not be true given the number of farm employees who may have more than one job or keep livestock at home. We then divide the monthly rates by 30 to determine the daily rates and multiply this daily rate by a probability that the indirect contact moves to another susceptible premises. Finally, we combine similar probabilities for efficiency's sake within the ISP (see Table 9). We then estimate the probabilities for different movement distances for indirect contacts from another table by the authors (see Table 10). The probabilities of transmission use the same function as the direct contact movements given above.

Table 9. Indirect Contact Rates. Green highlighted columns show the data or calculations we add to the corresponding table in Bates et al. (2001). We consider the numeric premises "Type Codes" from our data to be equivalent to the "Facility Types" from Bates et al. (2001). We calculate the Average Daily Movement Rate by multiplying the average daily indirect contact rate by the probability of a movement given an indirect contact. We then average similar movement rates in order to increase the efficiency of running the model in ISP. The second table below shows how these combinations were modeled in the ISP.

Indirect Contact Movement Rates									
Type Codes	Facility type	Employee	Friend	Mean Monthly Indirect Contacts	-95%CI	+95%CI	Mean Monthly Indirect Contacts (Removing Employees and Friends)	Avg Daily Contact Rate	Avg Daily Movement Rate
24,34,114,214,314	Backyard	4.2	18.2	26.1	15.9	36.3	3.7	0.1233	0.0123
310	Goat	39.9	3.0	50.6	0.0	137.2	7.7	0.2567	0.0257
211213	Sheep	8.1	14.4	30.5	16.4	44.6	8.0	0.2667	0.0267
	Beef								
51,61	< 250	9.0	9.3	22.1	13.7	30.5	3.8	0.1267	0.0127
53,63	>= 250	30.0	6.2	46.0	28.0	64.0	9.8	0.3267	0.0327
	Dairy								
31,32	< 1000	89.4	16.5	234.3	220.8	247.8	128.4	4.2800	0.4280
none	1000 - 1999	213.3	13.0	418.6	401.7	435.5	192.3	6.4100	0.6410
33	>= 2000	439.8	17.9	743.2	716.3	770.1	285.5	9.5167	0.9517
	Calf/heifer								
41	< 250	22.5	3.8	27.8	15.5	40.1	1.5	0.0500	0.0050
43,73	>= 250	463.2	17.0	609.4	128.3	1090.5	129.2	4.3067	0.4307
	Swine								
121,131,151,161	< 2000	76.2	9.4	97.9	36.0	159.8	12.3	0.4100	0.0410
153,163	>= 2000	750.0	1.7	807.3	374.9	1239.5	55.6	1.8533	0.1853
t =	30								
Probability of Movement|Contact =	0.1								

Type Codes	Spread Type Modeled By	Average Movement Rate
41	Mvmt 14	0.0050
24, 34, 114, 214, 314, 310, 211, 213, 51, 61, 53, 63, 121, 131, 151, 161	Mvmt 15	0.0252
153,163	Mvmt 16	0.1853
31,32,43,73	Mvmt 17	0.4294
33	Mvmt 18	0.9517

Table 10. Movement Distance Probabilities used to model indirect contacts. We estimate the probabilities for each of the specified distances from the corresponding table in Bates et al. (2001).

Probability for Specified Distance Travelled for Indirect Contacts						
Contact Type	9,000	19,000	29,000	39,000	49,000	59,000
AI Tech	0.627	0.263	0.042	0.059	0.000	0.009
Hoof trimmer	0.237	0.395	0.263	0.053	0.026	0.026
Vet	0.456	0.327	0.105	0.053	0.007	0.052
Avg. of Distance Travelled by Contact Type	0.440	0.328	0.137	0.055	0.011	0.029

We model the distribution of movements between farms and markets with a Poisson distribution with $\lambda = 0.1$, which equates to a movement from the farm to market about once every 10 days (i.e., 1 day divided by the rate of 0.1 per day). The probabilities for different movement distances are estimated from the graphs in Bates et al. (2001) and are shown in Table 11. The probability of transmission given a contact at a market is a constant 80% for our initial plausibility model.

Table 11. Movement Distance Probabilities used to model farm to and from market movements. We estimate these probabilities for each of the specified distances from the corresponding graphs in Bates et al. (2001).

Probability for Specified Distance Travelled Between a Premise and Sales Yard (Distance in Meters)									
Movement Type	**19,000**	**39,000**	**59,000**	**79,000**	**99,000**	**119,000**	**139000**	**159,000**	**179,000**
From Seller to Sales Yard	0.546	0.216	0.167	0.018	0.005	0.014	0.004	0.006	0.024
To Buyer from Sales Yard	0.383	0.202	0.119	0.061	0.013	0.069	0.04	0.021	0.092

b. Local Spread

ISP uses a spread mechanism called Local Spread to model short distance aerosol spread and spread between premises that cannot be specifically attributed to direct or indirect contact (Sanson, Stevenson, Mackereth, & Moles-Benfell, 2006b). "Through the fence" contact, or mechanical carriage of the virus by small domestic or wild animals, is an example of what Local Spread attempts to model. Sanson et al. (2006b, p. 3) writes that, "2160 out of the 2365 (91%) of the IPs in the U.K. 1967 – 1968 FMD epidemic were attributed to local spread, illustrating the perceived importance of this mechanism." We use Sanson, Stevenson, & Moles-Benfell (2006a) as our guide to setting the local spread initial settings, but increase the duration of the local spread from the four days in their research to five days. We also increased the probabilities of spread at each distance band in order to increase the spread of the disease after our initial testing showed significantly slower spread than some comparable models used in California. We show the settings used in the development of the model in Table 12.

Table 12. Probability of local spread of the virus at distance bands of 0–1 km, 1–2 km, and 2–3 km from the infected premises. We allow this spread to begin one day prior to and four days after clinical signs for the disease are evident on the premises.

	Local Spread Distance (m)		
Days After Clinical Signs	**1,000**	**2,000**	**3,000**
-1	0.013	0.003	0.001
0	0.039	0.009	0.003
1	0.052	0.012	0.004
2	0.052	0.012	0.004
3	0.052	0.012	0.004
4	0.052	0.012	0.004

ISP also has parameters within the Local Spread section for the relative susceptibility of different species to local spread. Donaldson et al. (2001) found that cattle are the most susceptible to the aerosol spread of the disease, followed by sheep and swine. We assume that goats and sheep are similar in their susceptibility and adjust the authors' findings slightly to account for the larger average cattle herd size in California. We set these parameters as guided by Sanson et al. (2006a) for cattle, swine, and sheep and goats to 1, 0.01, and 0.05, respectively, for our plausibility models.

c. Infectivity

This section within ISP includes a probability distribution describing the time between an animal's infection and when that animal starts to show clinical signs of infection. This is also known as the incubation period. From studying the 2001 U.K. FMD outbreak, Sanson et al. (2006b) determined that a good representation of the incubation period is given by the cumulative distribution shown in Figure 9, which we use in our plausibility model.

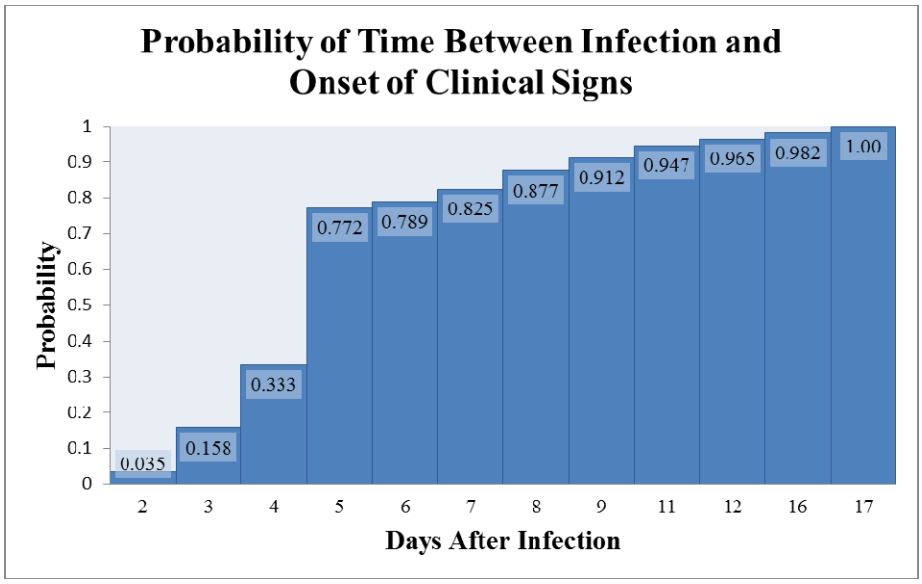

Figure 9. Cumulative distribution describing probabilities associated with the time between animal infection and the onset of clinical signs of the disease (Sanson, 2006b). All species use the same distribution.

The other parameter we used in the Infectivity section describes the variation of herd infectiousness over time. This parameter is multiplied by the probability of transmission parameters in the other sections to specify an overall probability of transmission. Sanson et al. (2006b) estimated this parameter by utilizing a Delphi conference of FMD experts. The participants at this conference determined that this parameter could be represented by a linear function decreasing from the 16th day after herd infection to the 33rd day after herd infection at a rate of 0.059.

4. Development of the Disease-Spread Control Parameters

Similar to Section 3, we wish to first check that our controlled spread model is plausible, so we initially set it up with mean or most likely parameter settings and test it to ensure that the disease control parameters are having an effect on the spread of the disease. ISP contains eight sections that model the control measures that may be undertaken to combat an outbreak of FMD. We do not model a statewide movement standstill, since this response is not specifically included in the CDFA FMD response plans (CDFA, 2006). The seven sections we use are listed below and described in the following paragraphs.

- *Zones*: apply to premises based on its modeling state and proximity to explicit boundaries or other premises
- *Surveillance*: models the detection of an infected premises
- *Resources*: applies constraints to the amount of depopulation or vaccination controls
- *Depopulation*: describes the depopulation strategy used by the model
- *Vaccination*: describes the vaccination strategy used by the model
- *Tracing*: models the detection of movements of the disease on or off a premise
- *Movement Restrictions*: describes how different movement types are restricted upon the first detection of an infected premise during the simulation

a. Zones

Similar to how ISP applies different modeling states to specific premises during the course of a simulation, ISP applies "Zones" to specific premises based on their geographic location. A user can define these zones explicitly using coordinate polygons or radially around a specific premise, in a specific modeling state. The user may also specify specific start and stop times for these zones, or have them triggered by a premise being assigned a specific modeling state. For our model, we use two explicit zones and three radial zones and describe them below:

- *ZoneCalifornia*: Explicit zone used to describe the boundaries of the modeling area, which is the state of California. We start this zone at the simulation start and keep it active for the entire simulation. This zone contains all premises in our dataset.
- *Zone_ControlArea*: Radial zone used to represent the Control Area and to define an area within a certain distance from a detected premise. If a premise is located in this zone, ISP will assign a model state of in_control_area and apply certain movement restrictions and surveillance methods to that premise as described below. Control area zones will be

active for the entire length of the simulation, beginning when the first premises are detected with the disease. The outside radius used for initial plausibility testing will be 10 km, which is the minimum radius recommended by the USDA for a control area (USDA, 2011).

- *Zone_Vaccinate*: Radial zone used to represent a Vaccination zone and to define an area within a certain distance from a detected premise. If a premise is located in this zone, ISP will assign a model state of in_vacc_zone and the premise will be added to a vaccination premises list, which will be described in the Vaccination paragraph below. Vaccination zones will be active for the entire length of the simulation, beginning when the first premises are detected with the disease. The USDA does not have a recommended radius for a vaccination zone, so we use 10 km as the outside radius for initial plausibility testing of the model.
- *Zone_Surv*: Radial zone used to represent the Surveillance Zone and to define an area within a certain distance from a detected premise. For premises located in this zone, ISP will assign a model state of in_surv_zone unless those premises are already in a control area. ISP will then apply certain movement restrictions and surveillance methods to those premises as described below. Surveillance zones will be active for the entire length of the simulation beginning when the first premises are detected with the disease. The outside radius used for initial plausibility testing will be 25 km, which is 5 km larger than the minimum radius recommended by the USDA for a control area (USDA, 2011).
- *Zone_likeDairy*: Explicit zone with the same boundaries as ZoneCalifornia above, but used to represent premises with a likeDairy modeling state. If premises are located in this zone, ISP applies certain movement restrictions and surveillance methods to those premises as described below. The likeDairy zone will be active for the entire length of the simulation.

b. Surveillance

ISP models the detection of infected premises using the Surveillance section of the control file. When a premises changes from an infected state to a detected state, authorities would assumedly impose some types of control measures to limit the disease spread. ISP uses two parameters to determine the likelihood of detection. The proportion of premises that participate in a surveillance type is called the *selection probability*, whereas the probability of an infected premise being detected, given that it is visited by a surveillance team, is called the *detection probability*. The detection probability can also be specified for each species modeled as desired by the user. We use Sanson et al. (2006b) and Hullinger (2012) as guides to these probabilities for the plausibility test of our model. Additionally, ISP models three rates within each type of surveillance:

- **Visit delay**, which is the rate at which the surveillance is delayed to a premise given it is selected for certain surveillance type;
- **Visit frequency**, which is the rate between visits while the premise is still on a surveillance list; and
- **Delay to detection**, which is the amount of time that passes between when a successful visit occurred on an infected premise and when that premise will be given the detected model state.

We show the surveillance parameter settings for our model in Table 13.

Table 13. Parameter settings for the seven Surveillance types within our model.

	Surveillance Type						
Parameter	**General Surveillance**	**General Surveillance After First Detect**	**General Surveillance - Dairy Before First Detect**	**General Surveillance - Dairy After First Detect**	**Control Area Surveillance**	**Surveillance Zone**	**Surveillance Trace**
Activation Option	Simulation start	time period	time period	time period	detected_farm	detected_farm	tracing
Time Period	Simulation start to first detection	First detection to simulation end	Simulation start to first detection	First detection to simulation end	First detection to simulation end	First detection to simulation end	First detection to simulation end
Surveillance Farm State			likeDairy_before Detect	likeDairy_after Detect	in_control_area	in_surv_zone	
Selection Zone	ZoneCalifornia	ZoneCalifornia	likeDairy	likeDairy	Zone_Control Area	Zone_Surv	ZoneCalifornia
Selection Probability	0.65	0.85	0.999	0.999	0.99	0.9	0.75
Visit Delay - Poisson	6	4.5	1.75	1.25	2.75	3.5	4
Visit Frequency - Poisson	6.5	4.5	1.75	1.25	4	4.5	4
Delay To Detection - Poisson	4.5	3	3	1.75	1.25	1.5	3
Detection Relative To	Clinical Signs	Clinical Signs	Clinical Signs	Clinical Signs	Clinical Signs	Clinical Signs	Clinical Signs
Detection Probability - Constant	0.495	0.895	0.745	0.895	0.895	0.895	0.895
Detection Probability (sheep) - Constant	0.475	0.825	N/A	N/A	0.825	0.825	0.825

c. Resources

ISP uses the Resources section in the control file to apply constraints to the control strategies specified by the user. If ISP needs to apply control strategies to a premise based on its current model state, that premise is added to a resource list. Then, ISP will be allowed to apply the required strategy to premises on the list at the rate specified within the resource section. ISP allows these strategies to vary over time, and we use a 10-day "ramp up" period for both vaccination and depopulation control strategies. During the first to the ninth day after a premise has been added to a resource list, we limit the control strategy to only 10% of the total amount of resources available during the rest of the simulation. For example, in our plausibility testing, we use a constraint that states that 20,000 animals can be vaccinated or depopulated per day at full utilization. So, on days 1 through 9, only 2,000 animals can be vaccinated or depopulated per day. The full utilization rate assumes that California has an equivalent amount of resources to depopulate as the U.K. did in 2001.

d. Depopulation

In the next section of the control file, we define our depopulation strategy, which is to only depopulate premises that have had the disease detected on them. ISP allows alternative preemptive depopulation in zones, usually in a radius around detected

premises, but we chose not to model this control measure because of our understanding of the current views in California to such a practice (Hullinger, 2012). The parameter settings we use are to activate a depopulation action upon ISP assigning a premise to the modeling state of "detected" and the action will only be applied to that particular premise. We will constrain this action using the depopulation resource described above.

e. Vaccination

Our vaccination strategy for the plausibility test is to vaccinate likeDairy premises that are assigned to the vaccination zone. Vaccinations are completed from the outside to the inside of a radial vaccination zone and are constrained by the resources described in the "Resources" paragraph above. Once a premise is vaccinated, its probability of infection by another premise is reduced, based on a user-defined lookup table. This table defines the proportion of animals on the premise that are not immune to infection at a given point in time. We use conservative estimates of this proportion, which we derived from Doel et al. (1994). The authors examined the rate of development of immunity in several FMD susceptible species, including cattle, and found that all of the cattle they tested were immune four days after vaccination. However, they also cite other studies that indicated that this result may be optimistic. Our table states that 10% of the animals on the premises are not immune after four days and 0.5% are not immune after 15 days. The effect of this proportion is that ISP multiplies the probability of transmission by this proportion to determine a new overall probability of transmission. For example, if a certain infected premise attempted to spread the disease to other premises that were in their fifth day after vaccination, ISP would multiply the calculated probability of transmission (e.g., 0.5) by 0.1, the number in the table, to reach an overall probability of transmission of 0.05.

f. Tracing

This is the attempt to find contacts that have been made onto or off of a particular detected premise. ISP can model both types of tracing, backward and forward. Backward tracing involves interviewing the staff of a certain detected premise to determine what direct and indirect contacts were possible between the start of the

outbreak and the presumed date of the premise's infection, which is based on the observation of the clinical signs of the disease. The goal of backward tracing is to determine what premises could have infected the detected premise and then to apply certain controls or surveillance to the possibly infected premise. In contrast, the goal of forward tracing is to determine what other premises that the detected premises could have infected since the presumed date of infection. This is accomplished in the same manner as backward tracing, by personal interview of the staff of the detected premise.

The ISP user can define tracing parameters for forward and backward tracing for each individual movement type or define them globally for all movement types. We apply the settings globally within our model. The tracing parameters available include: when the tracing action will begin, the probability that a movement is forgotten, and the rate at which tracing interviews are accomplished. We use all of these parameters as described below:

- *Time period to start tracing*: We begin tracing operations two days after the first detection and continue them through the entire simulation.
- *Probability the movement is forgotten*: We use a setting of 42.5% of movements will be forgotten.
- *Tracing delay*: We use a Poisson distribution with a mean rate of delay of 3.75 for this setting. This equates to having to an average time until tracing is complete of almost four days.

g. Movement Restrictions

ISP reduces the rate for each movement type after the first infected premise is detected using the movement restriction parameters within the control file. For our model, we define three movement restrictions. For all movement types with a source or destination premise in a control area, the probability that the movement will not occur is set to 92%. For all movement types with a source or destination premise in a surveillance zone, the probability that the movement will not occur is set to 84.5%. We added an additional movement restriction on all to or from market movement within California in order to test that control strategy. This restriction is turned on or off by

setting the probability that the movement will not occur to either 0% or 99%, depending on the strategy used. For our plausibility testing, this probability was set to 0%, meaning that only markets in a control area or surveillance zone are affected by a movement restriction.

5. Development of Starting Scenarios

As mentioned earlier, the majority of the studies conducted on the spread of FMD in California have been limited to the Central Valley of the state, where the majority of the large livestock premises are located. We wish to broaden that scope by starting outbreaks of the disease randomly chosen from all premises in California if they meet certain conditions. The conditions we choose are based on the suspected sources of FMD outbreaks of modern livestock countries as well as expert opinion (Hullinger, 2012 & Stevenson, 2012). We show the scenarios we model in Table 14.

Table 14. Description, methodology, and rationale behind the scenarios we model.

Scenario	Description	Methodology	Rationale
Southern Border	Randomly infect five cattle facilities along the southern border of California to represent spread from a Mexican FMD outbreak.	If [(Latitude <= 33 or Longitude >= -115) And number of Cattle on Farm > 10], then eligible for selection. Randomly selected 5 initially infected premise from eligible list.	Bulgaria, 2011. Index case was near the Turkish border and a feral pig was antemordem diagnosed with FMD. Turkey had an FMD outbreak occuring at the time.
Market	Randomly infect one market to represent spread from direct or indirect contact.	If Type = 511 OR 512, then eligible for selection. Randomly select 1 to be initially infected premise.	Markets are known to be supernodes in the spread of FMD. The source of infection to the market could have been a person involved in the livestock industry who had recently returned from travel to a country with a current FMD outbreak.
San Francisco Port	Randomly infect one swine facility near San Francisco to represent illegal import of feed for swine (as in UK outbreak of 2001).	If [(37.25 < Latitude <= 38.25 And Longitude < -121.75) And number of Swine on Farm > 10], then eligible for selection. Randomly selected 1 initially infected premise from the eligible list.	Swine infected by feeding on illegally imported meat were the probable sources of infection in Taiwan (1997), the UK (2001), and South Korea (2011)
LA Port	Randomly infect one swine facility near Los Angeles to represent illegal import of feed for swine (as in UK outbreak of 2001).	If [(33.2 < Latitude <= 34.2 And Longitude < -117) And number of Swine on Farm > 10], then eligible for selection. Randomly selected 1 initially infected premise from the eligible list.	
High Animal Density	Randomly infect one cattle facility in an area in the 90th percentile or higher of animal-dense locations.	If [(Number of Animals within 10k > 47779 (90th Percentile)) And (Latitude > 34) And number of Cattle on Farm > 10)], then eligible for selection. Randomly selected 1 initially infected premise from the eligible list.	Conducted in order to compare our model to other models of FMD in California, most of which are in high animal dense areas. Also, this is the most likely area to be infected by an terrorist organization.
Low Animal Density	Randomly infect one cattle facility in an area in the 10th percentile or lower of animal-dense locations.	If [(Number of Animals within 10k < 647 (10th Percentile)) And (Latitude > 34) And number of Cattle on Farm > 10)], then eligible for selection. Randomly selected 1 initially infected premise from the eligible list.	Conducted to contrast with the High Animal Density Scenario.
High Premise Density	Randomly infect one cattle facility in an area in the 90th percentile or higher of premise-dense locations.	If [(Number of Farms within 10k > 185 (90th Percentile)) And (Latitude > 34) And number of Cattle on Farm > 10)], then eligible for selection. Randomly selected 1 initially infected premise from the eligible list.	Conducted in order to determine how ISP reacts to high premise dense areas in comparison with high animal dense areas. This may also indicate how the disease could spread through Northern California, which is a geographic area which has not been studied as much as other areas of the state.
Low Premise Density	Randomly infect one cattle facility in an area in the 10th percentile or lower of premise-dense locations.	If [(Number of Farms within 10k < 12 (10th Percentile)) And (Latitude > 34) And number of Cattle on Farm > 10)], then eligible for selection. Randomly selected 1 initially infected premise from the eligible list.	Conducted to contrast with the High Premise Density Scenario.

III. PLAUSIBILITY TESTING OF INITIAL DISEASE-SPREAD MODELS

In this chapter, we describe and compare the disease-spread dynamics of the Uncontrolled and Controlled Spread Models described in Chapter II. Testing model plausibility is difficult because no outbreaks of FMD have been observed in California since 1929, and the livestock industry has changed considerably since then. We therefore have two options to use in order to attempt to categorize our simulation model as plausible or not.

- First, we could attempt to study recent outbreaks in countries whose livestock industry is similar to ours and parameterize our model similar to how those outbreaks actually behaved. This method, however, ignores important differences between California and those countries in animal husbandry methods, animal/premises densities, and intensity of operations.
- Second, we could consult a number of subject matter experts (SME) to try to discern how to parameterize the model based on their opinions as Sanson et al. (2006b) did when parameterizing ISP for New Zealand. This method is also difficult because SMEs do not always agree, it may not be clear how to weight differing opinions, and it is time consuming to gather and compile the opinions.

Of these two, the SME option may be a better course. Because of time availability, however, we choose to compare our simulation model to another country's outbreak. Ultimately, this plausibility test does not have much impact on our final results because we use a design of experiment to explore a wide variety of different parameter combinations in order to see which are most important in the model. The plausibility testing that we conduct here is merely done to ensure that the model is producing reasonable results and should not be construed as being predictive of an actual outbreak of FMD in California.

A. THE UNCONTROLLED SPREAD MODEL

In order to determine whether the base models we developed are plausible, we begin by comparing the uncontrolled spread model to the "silent spread" of the disease—the spread of the disease prior to infected premises being detected—from a previous outbreak in a modern livestock country. Gibbens et al. (2002) estimated that during the U.K. outbreak in 2001, at least 57 premises were already infected with FMD when the first detected case was disclosed. Using the starting scenarios described in Section 5, we compare how many premises were infected on the 21st day of our model to the author's estimated number of premises in order to determine our model's plausibility. Even though some of the starting scenarios had significantly larger outbreaks, we believe that the model we developed is plausible because the average across all scenarios tested was similar to the U.K. outbreak, and two of our scenarios were within 11 premises of the U.K. number. The results of this comparison are shown in Table 15.

Table 15. Six out of seven scenarios we examined that are similar to the 2001 U.K. FMD outbreak have an average outbreak size after 21 days that are in the same order of magnitude as the U.K. outbreak, which had an estimated 57 infectious premises on the 21st day of the outbreak (Gibbens et al., 2002). We conclude from this comparison, that our model is a plausible model of uncontrolled spread within California.

Number of Infected Premises by Scenario (100 Iterations)				
Scenario	**Mean**	**Std Dev**	**Q.25**	**Q.75**
Low Animal Density	10.40	20.45	1.00	8.00
Border	60.47	30.00	38.25	77.75
Market Start	14.92	57.67	1.00	5.75
LA Port	12.34	10.50	5.25	15.75
SF Port	537.38	143.43	450.25	572.75
High Premise Density	68.59	83.02	16.00	95.00
Low Premise Density	11.18	66.12	1.00	1.00
All Scenario Average	102.18	58.74	73.25	110.86

We also looked at which spread mechanisms were causing the disease spread to see if those mechanisms were similar to the literature. The mechanisms that were causing the most spread were MovementType12, which is market movement; MovementType18, which is indirect contact from large dairy premises; and local spread (see Figure 10). Even though the local spread effects may be higher than expected when compared to the indirect contact and market movement, especially when considering that many forms of indirect contact are catagorized as local spread within actual outbreak statistics, we feel these spread mechanisms are similar in their impacts on the outbreak to those observed in the literature and are therefore plausible for our purposes.

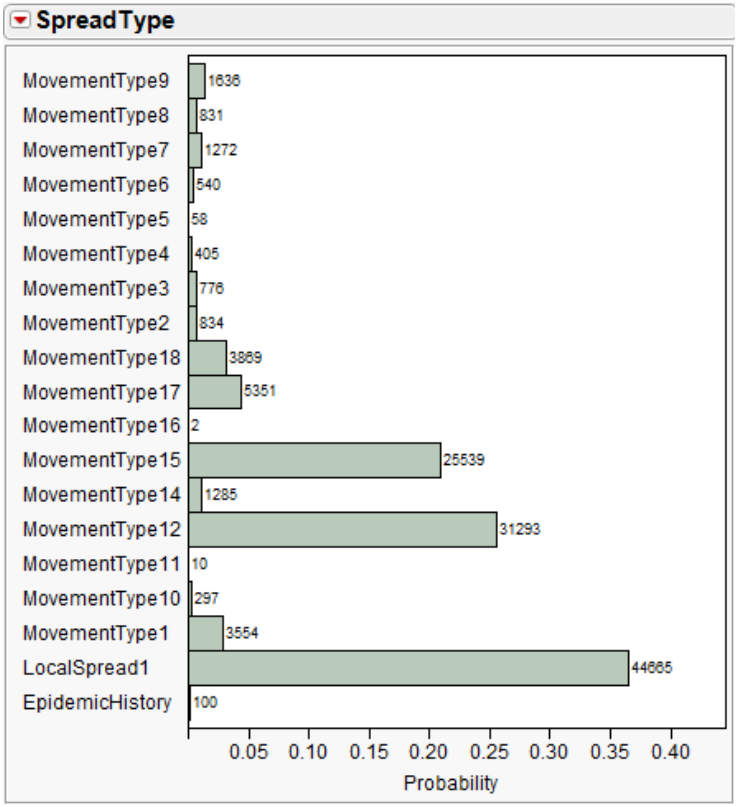

Figure 10. The distribution of disease-spread mechanisms during plausibility testing of the Uncontrolled Spread Model. The spread mechanisms with the highest probability of causing disease spread are MovementType12, which is market movement; MovementType15, which is indirect contact at many types of premises; and local spread. The x-axis shows the probability that the spread mechanism shown along the y-axis causes disease spread. The counts to the right of each bar show how many times the spread mechanism caused the disease spread over the 100 iterations that the simulation was run. See Appendix A for the details of each spread type.

B. THE CONTROLLED SPREAD MODEL

Determining the plausibility of the controlled spread model is more difficult than the uncontrolled model, since the controls used are unique to what we believe are "most likely" control scenarios for the United States and, as such, are not comparable to outbreaks in other countries. In order to determine plausibility, we simply observe how the uncontrolled spread model is affected by the same set of controls over all starting scenarios to ensure that the outputs are reasonable. We found that the control parameter settings affected the uncontrolled spread model predictably for all scenarios. An example showing the spread comparison between models, using the High Premises Density scenario, is shown in Figure 11, and the distribution of spread mechanisms is shown in Figure 12.

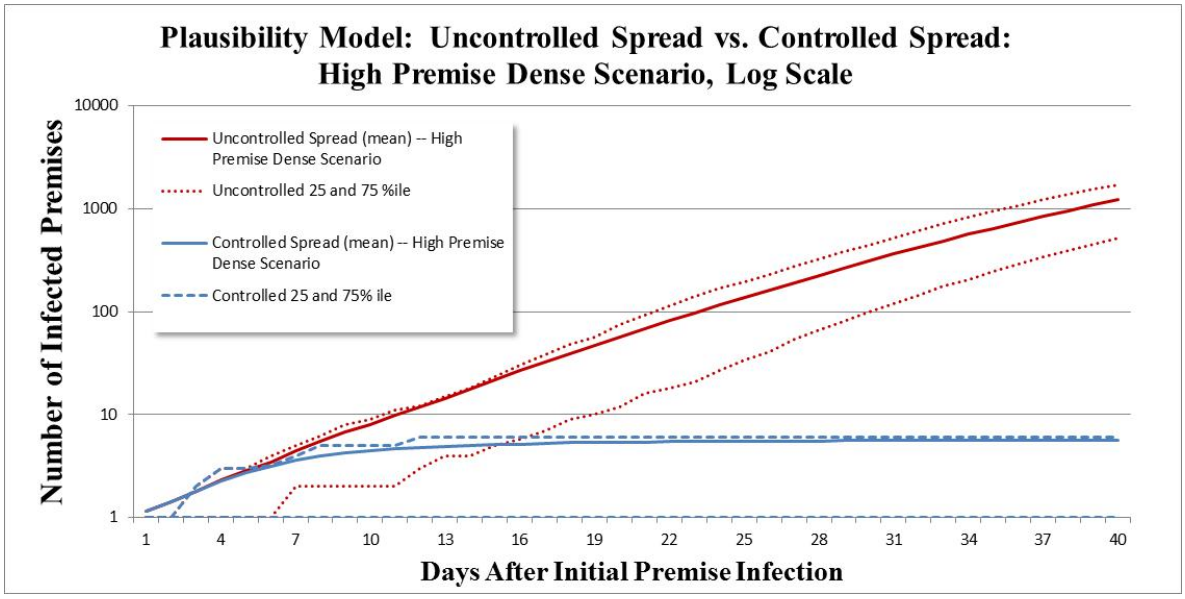

Figure 11. Comparison of Plausibility Models: Uncontrolled Spread vs. Controlled Spread. By observing the infected premises curve for both the uncontrolled and the controlled spread on a log scale, we can see the effect of detecting an infected premise. Here, the minimum detection time over 100 simulation iterations was two days, but the effect of the detection begins on Day 4, based on the length of time needed to apply controls.

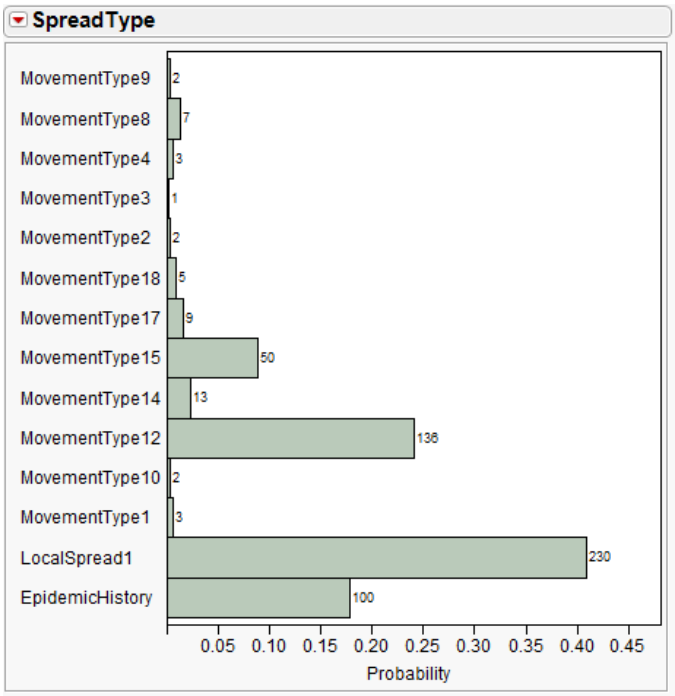

Figure 12. The distribution of disease-spread mechanisms during plausibility testing of the Controlled Spread Model. The spread mechanisms with the highest probability of causing disease spread are local spread and MovementType12, which is market movement. Notice that Epidemic History, which is merely the initially infected premises, contains almost 20% of the spread and how the counts along each bar are significantly reduced from Figure 10, which indicates that the controls are having an effect on the disease spread.

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IV. SIMULATION EXPERIMENTAL DESIGN

Because intentionally introducing the virus into a large livestock population is not a viable method for scientific inquiry, FMD is generally studied in one of three ways:

- **Live virus** infection and study of a limited quantity of susceptible animals to determine virus and vaccine characteristics;
- **Statistical studies** of past or current outbreaks to study how diseases have spread through populations, given the characteristics of the study area and virus type/subtype; and
- **Simulation modeling** to attempt to predict the characteristics of future outbreaks.

We intend to use the research completed by others in the first two ways to inform our research of the third way—simulation modeling. We do this by designing an efficient experimental design that varies the parameters of the simulation in order to find response strategies that are robust to those variations. The next section explains how this was done by giving an overview of why we use an experimental design in general, and then how we implemented our design specifically.

A. WHY WE USE AN EXPERIMENTAL DESIGN

In Chapter II, Section A, we described some of the objectives of simulation modeling of a disease. There exists significant uncertainty in the way that a disease spreads through a population; the manner in which the first premises are infected; and what policies, technologies, and logistical constraints we may have in our attempts to control the disease. In order to study how the disease may spread and to find control measures that are robust to these uncertainties, we run the simulation many times using a variety of simulation parameter settings, initial infection scenarios, and control strategies. With 73 factors considered in our model, conducting a full-factorial design—one that tries every combination of factors—is computationally intractable. Even by making every factor binary, having only a high and low setting, it would require 2^{73} simulation

runs. Instead, we conduct this experiment in an intelligent way in order to maximize our insights and conclusions. So, we use an efficient experimental design. As Sanchez (2008, p. 73) states,

> …for those interested in exploring the I/O (Input/Output) behavior of their simulation model, efficient experimental design has a much higher payoff at a much lower cost. A well-designed experiment allows the analyst to examine many more factors than would otherwise be possible, while providing insights that cannot be gleaned from trial-and-error approaches or by sampling factors one at a time.

An experimental design is a matrix in which every row represents one simulation run, called a *design point*, and every column represents a certain parameter, called a *factor*. In our case, the factors include the different ways the disease could behave, the environment in which the disease starts and spreads, and the controls we impose to stop that spread. Examples of the factors we look at in the experimental design include: the rate at which animals start to show clinical signs of FMD, the probability of an animal being moved some distance and spreading the disease, and how often animals are observed for signs of the disease. Our goal is to then test the factors at many different settings, called levels, in an efficient way that allows us to see the factor levels' effects on the spread of the disease without undue strain on our computational resources.

Many experimental designs for simulations exist in the literature and several have been designed at the Naval Postgraduate School's Simulation Experiments and Efficient Design (SEED) Center. Most of these designs are based on nearly orthogonal Latin hypercube (NOLH) designs and may be crossed with a traditional factorial design to make a mixed design (Cioppa & Lucas, 2007). NOLH designs have good qualities in that they are "space-filling" and have minimal pairwise correlations between factors. The former is beneficial because it explores the entire sample space and the latter because it ensures that the metamodel developed from the design will indicate factor coefficients very similar to the true, unknown, coefficients—even in the presence or absence of other more significant factors. In other words, even if the factors we include in our experiment are not the most significant factors impacting the simulation output, the metamodel is still

informative because it shows the correct main effects of included factors. It cannot, however, show the interactions of the included factors with the factors we choose not to include.

B. OUR EXPERIMENTAL DESIGN IMPLEMENTATION

Because of the complexity of ISP and its large number of inputs, attempting to analyze the ways in which these inputs affect the output of the simulation is a significant endeavor. We use a Nearly Orthogonal and Balanced design for our experiment (Vieira, 2012a). From ISP, we choose 70 continuous and 2 discrete two-level parameters to vary. We then cross this design with the eight starting scenarios to develop 4,096 unique design points. We show a small sample of the design in Figure 13 and a description of each factor in Appendix A. The design has a maximum pairwise correlation of less than 4%. Five percent is the maximum to still be considered a nearly orthogonal design. For each design point, we generate an ISP control file and an epidemic history file with randomly chosen, initially infected premises based on the constraints of the modeled starting scenario. Each control file is used to simulate 100 iterations, for a total of 409,600 individual simulations. The simulations were run on the SEED Center's cluster of 60 computers and took approximately seven days to complete.

low level	x	0.01	0.862	0.25	0.1	0.5	0.25
high level	x	2.034333333	1.041333333	2	0.5	1	2
decimals	x	4	4	4	4	4	4
factor name	EpidemicHistory:StateFileName	MovementType17:NumberPerTimePeriod[31|32|43|73]	MovementType18:NumberPerTimePeriod[33]	AllMovements:MovementDistance	AllFarms:ProbabilityOfTransmission	AllMarkets:ProbabilityOfTransmission	LocalSpread1:Multiplier
1	.\STATE_Animal_High.txt	1.8244	0.922	1.3664	0.1008	0.7446	1.5856
2	.\STATE_Animal_High.txt	1.8204	1.0199	1.0479	0.4162	0.6507	0.8459
3	.\STATE_Animal_High.txt	1.9868	0.9645	1.0548	0.4115	0.5949	1.1815
4	.\STATE_Animal_High.txt	1.147	0.889	0.3048	0.1266	0.6468	1.4966
5	.\STATE_Animal_High.txt	1.0756	1.0319	0.8699	0.1806	0.9247	0.9041
513	.\STATE_Animal_Low.txt	1.8244	0.922	1.3664	0.1008	0.7446	1.5856
514	.\STATE_Animal_Low.txt	1.8204	1.0199	1.0479	0.4162	0.6507	0.8459
515	.\STATE_Animal_Low.txt	1.9868	0.9645	1.0548	0.4115	0.5949	1.1815
516	.\STATE_Animal_Low.txt	1.147	0.889	0.3048	0.1266	0.6468	1.4966
517	.\STATE_Animal_Low.txt	1.0756	1.0319	0.8699	0.1806	0.9247	0.9041
1537	.\STATE_Port_LA.txt	1.8244	0.922	1.3664	0.1008	0.7446	1.5856
1538	.\STATE_Port_LA.txt	1.8204	1.0199	1.0479	0.4162	0.6507	0.8459
1539	.\STATE_Port_LA.txt	1.9868	0.9645	1.0548	0.4115	0.5949	1.1815
1540	.\STATE_Port_LA.txt	1.147	0.889	0.3048	0.1266	0.6468	1.4966
1541	.\STATE_Port_LA.txt	1.0756	1.0319	0.8699	0.1806	0.9247	0.9041

Figure 13. Screenshot from the experimental design with the first five design points of the first three starting scenarios. The six factors shown are varied in a nearly orthogonal and balanced way between the low and high levels shown in the first two rows of the spreadsheet.

C. MEASURES OF EFFECTIVENESS (MOE)

There are many ways to measure how effective the control policies implemented during an outbreak are in terms of their impact on the livestock industry and the animals on the premises. Depending on the priorities and costs involved with a particular outbreak, some authorities will be most concerned with the number of animals or premises infected, while others will care more about how many of either are vaccinated, depopulated, or put under some type of movement restriction. For our analysis, we focus on those measures of effectiveness (MOEs) we feel have the most impact on the livestock industry and the state of California:

- **Detection Time**: the amount of time between the start of the simulation and when the first infected premises are detected.
- **Infected**: the number of cattle or premises infected. We include cattle in this MOE because it is the animal that has the most impact on the economy in California.
- **Affected by Movement Restrictions**: the number of cattle or premises affected by movement restrictions, either in the control area or surveillance zone. We include this because movement restrictions pose an economic burden on premises in the control area. We view this MOE as as a surrogate to explicitly modeling the economic impact, which would require significantly more research and detail in the model to be accurate.
- **Weighted Average of Infected and Affected**: Sixty percent of the weight was given to Infected and 40% to Affected, signifying that infected premises are more detrimental to the study area than affected premises. This MOE allows us to combine the previous MOE in order to see if controls can be effective against both simultaneously.
- **Frequency of Max Infected Premises:** the number out of 100 simulation iterations reaching the maximum infected premises limit. This MOE helps us determine the potential for a large outbreak.

We considered four ways of calculating each MOE, with the exception of the Frequency of Max Infected Premises, which is measured by a simple count. The first

way is the mean over all simulation iterations. This is the simplest and most easily explainable method to describe the data; however, it does not account for any variability displayed within the simulation and may oversimplify the characteristics of the outbreak. Some modelers prefer using the median instead of the mean because the distributions of the output variables in most FMD models are highly skewed. The median is a better predictor of what would be most often seen of the MOE. We prefer the mean, however, because our purpose is to limit "worst-case" outbreaks, which we believe are not modeled as well by the median. The second way is the upper quartile mean. This statistic is calculated by taking the mean of the upper quartile of the simulation results and is a more pessimistic view of the data than the mean, since it only includes the largest 25% of the outbreaks represented by a design point. It provides a better measure to compare control strategies aimed at limiting large outbreaks while not being overly influenced by outliers. Like the mean, it does not expressly measure the variability of the output, though. The final way we consider is to calculate the MOE by using a quadratic loss function, which is the sum of the mean squared and standard deviation squared; a standard measure in simulation analysis (Sanchez, 2000).

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V. DATA ANALYSIS

In this chapter, we describe the results of our simulation model and the analysis of the data. We leave our interpretations and conclusions from each result for Chapter VI. Primarily, we use JMP Pro 9.0 (JMP, 2012) as the statistical software package to conduct our analysis. When describing the factors within our model, we use the term "decision factor" with factors that are controlled by livestock producers, livestock-related individuals or companies, or state or federal authorities before or during an FMD outbreak. Examples include the size of a control area or a particular vaccination strategy. Alternatively, we use the term "noise factor" with factors that are not controlled or only controlled at a significant cost, such as the average time until clinical signs are apparent or the number of animal movements that originate at small dairy premises prior to the detection of an outbreak. We do not describe each factor modeled in detail in this chapter. Instead, we provide these detailed descriptions in Appendix A. We divide the chapter into six sections:

- **Correlation:** a description of how the factors correlate with the MOEs and how the MOEs correlate with each other.
- **Models used to explore simulation output:** descriptions of the modeling techniques we use to explore the simulation output.
- **Impact of starting scenarios:** a description of how the starting scenarios impacted the simulation results.
- **Time until the first detection of infected premises:** a description of the detection time results and the models we use to determine its contributing factors.
- **Mean number of infected premises:** a description of the number of infected premises results and the models we use to determine this MOE's contributing factors.
- **Model to explore the potential for a large outbreak:** a description of the model we develop to address the impact of the maximum number of infected premises parameter within our simulation.

A. CORRELATION

Correlation is an indicator of the linearity in the relationship between two factors. (Montgomery, Peck, & Vining, 2006). It is a number between –1 and 1, with negative numbers indicating that as one factor grows, the other decreases. It should not be used to predict the value of one factor given another factor, but can be valuable as a first step towards looking for relationships between two factors and getting an idea of how well predictive models may perform. We produce a correlation matrix in order to check the pairwise correlations between all of the factors and MOEs within our model and provide our analysis in the next three sections.

1. Factor and MOE Correlation

Correlations between the factors and MOEs are generally between –0.25 and 0.25, with only two exceptions. The first is the Local Spread Multiplier, which is a noise factor. This is a multiplier applied to the distance bands of the local spread parameter within ISP (see Table 12). For example, the distance bands used in the base model for Local Spread are 1,000 m, 2,000 m, and 3,000 m. The Local Spread Multiplier varies these bands through multiplication. Thus, if a Local Spread Multiplier of 1.5 was applied to a specific design point, then the resulting distance bands would be 1,500 m, 3,000 m, and 4,500 m. The probability of the disease spread to those distance bands would remain the same, however. The Local Spread Multiplier was correlated at 0.25 or above to all MOEs except Average Detection Time and Robust Weighted Average of Infected Cattle. This indicates that as the Local Spread Multiplier increases, so would the MOE. The second factor showing some correlation is the Delay To Detection of Dairy or Dairy-like Premises, which describes the amount of time between when a certain premises is inspected for disease and when the disease is actually detected. This factor is positively correlated with the Average Detection Time at 0.53.

2. Impact of Factor Correlations on Potential Models

Since the correlations between both the noise and decision factors with the MOE are low, we suspect that there is significant nonlinearity within the simulation output (see

Figure 14), and that no simple linear or quadratic functions will represent the outbreaks with high confidence. This is to be expected, however, within a complex system such as disease spread. Keeling (2005, p. 1196) states,

> For the spread of FMD, existing biological and veterinary knowledge is still not sufficiently quantified to enable the creation of a complex model that can accurately encompass all the mechanisms of disease transmission both within and between farms, and more basic research is needed.

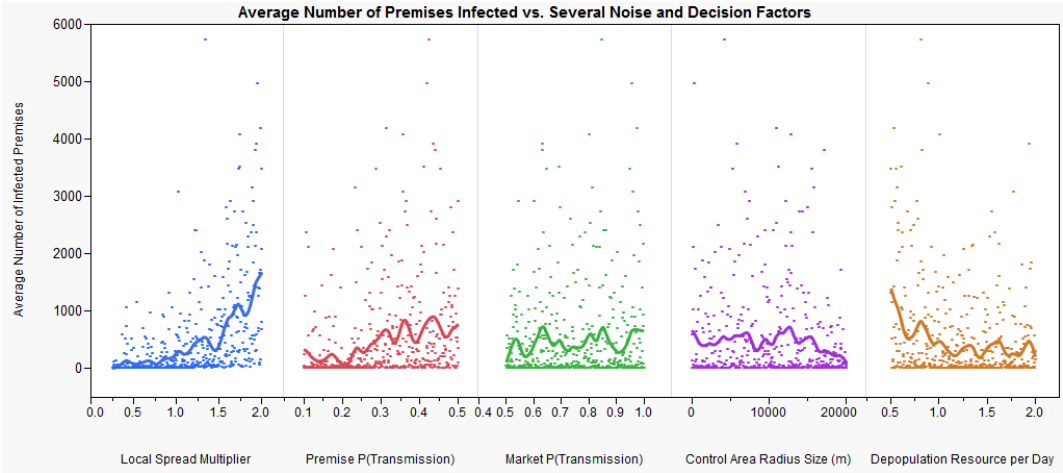


Figure 14. Average Number of Premises Infected vs. Several Noise and Decision Factors. The relationship between the MOEs and each of the factors is not clearly linear and there exists a large amount of variation within the data.

3. Between MOE Correlation

Correlations between all MOE pairs, with the exception of Detection Time, are generally above 0.8. This indicates that the MOEs are highly positively correlated. We show a sample of the effect of a high correlation in the graph in Figure 15. Because of the similarity between MOEs, for simplicity's sake, we will generally discuss our simulation results using the mean of the MOEs.

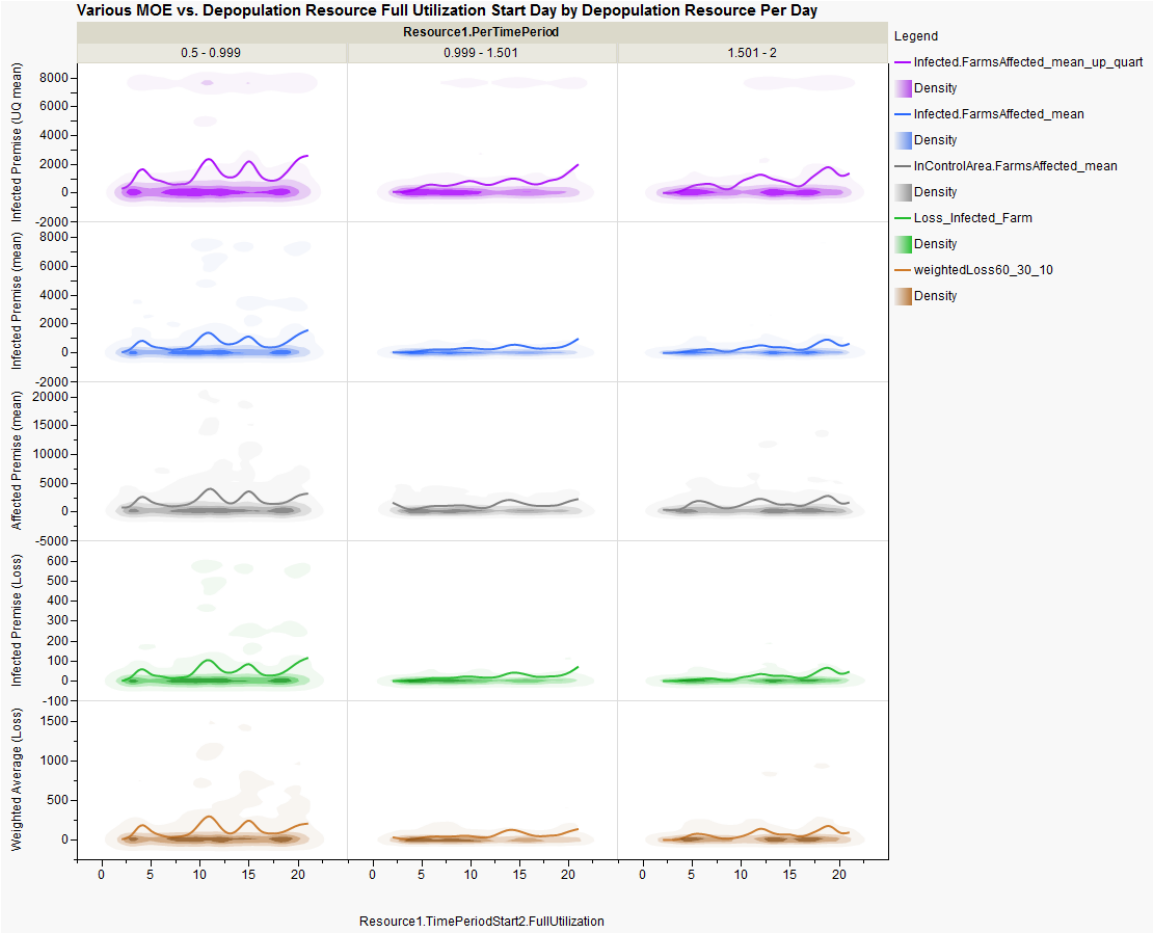


Figure 15. Graphs showing how similar various calculations of MOEs are when plotted against the same variables—here two depopulation resource factors. The vertical axis describes several different MOEs. The horizontal axis within each column describes a change in the "Resource1.TimePeriodStart2.FullUtilization," which is the number of days until all depopulation resources are available. Each column of graphs represents a bin for the "Resource1.PerTimePeriod," which is the full number of resources available for depopulation. The smoother lines in each column of graphs, where the MOE changes, but the factors vary similarly, are virtually identical. This is the effect of having highly correlated MOE.

B. MODELS USED TO EXPLORE SIMULATION OUTPUT

We use two common techniques to model the output of our simulation: multiple-regression analysis and partition trees, also known as classification and regression trees

(CART). Both of these will be impacted by low correlations between the factors and the MOEs, and by the suspected nonlinearity within the simulation. Below are descriptions of the two techniques.

1. Multiple Regression Analysis

Multiple regression analysis seeks to explore the relationship between several factors, called regressors, and a response variable, which we call an MOE (Montgomery, Peck, & Vining, 2006). It does this by attempting to approximate the behavior of the response variable with a linear equation incorporating the regressors. By observing the coefficients of the linear equation, we are then able to identify which factors have the greatest impact on the response variable or MOE. We evaluate the models using the adjusted R^2, a common measure to compare how models are able to describe the data. This statistic is a score between 0 and 1 that measures how much variability is explained by the factors in the model, but penalizes for adding insignificant factors to the model (Montgomery, Peck, & Vining, 2006). In order for the regression to be adequate, four assumptions about the residual errors between the actual response and the predicted response must be met. They are: the mean of the errors must equal zero, the errors must have constant variance, all errors are independent, and all errors are normally distributed. The most difficult of the assumptions for us to meet is the normality assumption because tests for normality are highly influenced by outliers, which are prevalent within our simulations. We will test all of these assumptions for the models presented later in this section.

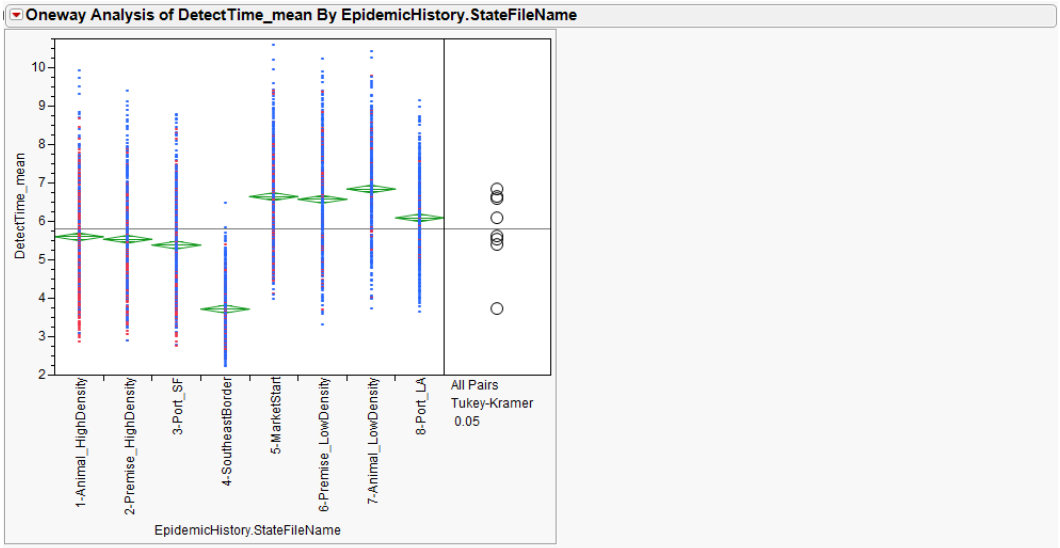
2. Partition Trees

Partition trees are graphical representations of a hierarchy of questions asked of the data to determine how they should be classified or grouped (Montgomery, Peck, & Vining, 2006). The questions are displayed as an upside down tree, with the root at the top containing the entire dataset. The data are then split sequentially in order to maximize the difference in the mean of continuous factors or the probability of categorical factors so that the nodes, or leaves, are as much alike as possible. Many

algorithms exist to accomplish these splits. JMP uses a log Worth calculation for categorical factors and a Sum of Squares (SS) calculation for continuous factors (SAS, 2010).

C. IMPACT OF STARTING SCENARIOS

Since ISP is a spatial model, we expect that it will behave differently given different starting scenarios, and that some scenarios are more likely to produce long detection times or large outbreaks. We tested these assumptions by conducting Tukey-Kramer HSD (honestly significant difference) comparison of means tests (Mendenhall & Sincich, 1984) on the Detection Time mean and the Infected Premises mean. This test calculates a single statistically significant critical difference (the HSD), in our case at a 95% confidence level, for the mean pairs and then groups the factor means in bins according to the computed critical difference. The results show that there are significant differences in the behavior of the model, based on a starting scenario using both MOEs. The Southeast Border scenario has a statistically significant lower mean detection time, while the High Animal Density scenario has a statistically significant higher mean number of infected premises. These results are shown in Figures 16 and 17. Additionally, all multiple-regression models and partition trees explained in Sections D, E, and F are first run with the starting scenario allowed in the model. In all cases, it is the most significant factor in the model. We present the rest of our models without the contribution of the starting scenarios, however, in order to focus on which factors contribute most to the MOEs across all starting scenarios.



Means Comparisons

Comparisons for all pairs using Tukey-Kramer HSD

q*	Alpha
3.03247	0.05

Abs(Dif)-HSD

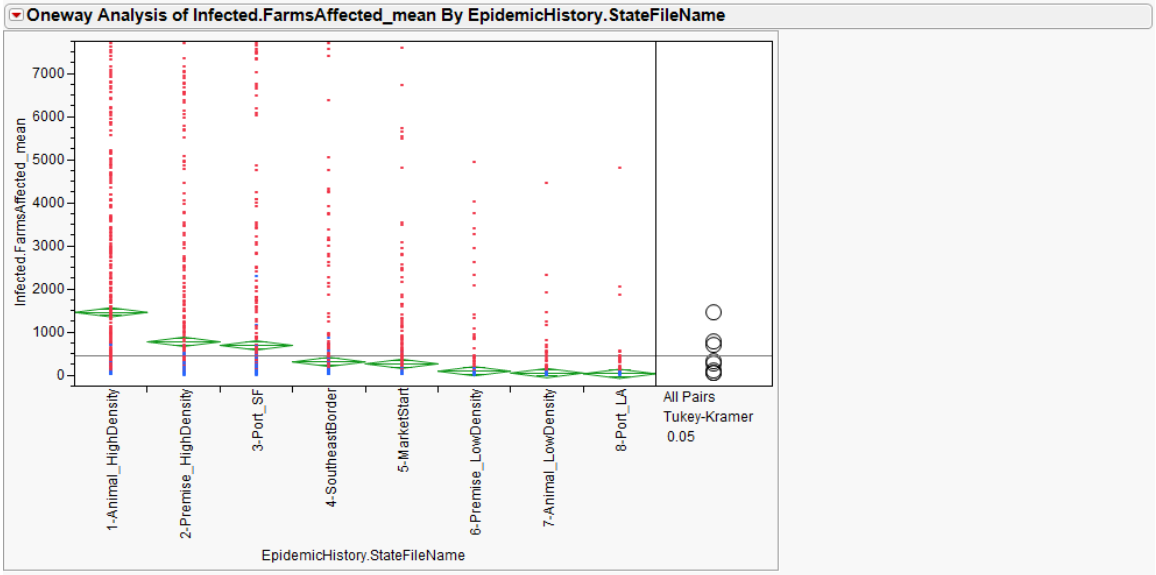
	7-Animal_LowDensity	5-MarketStart	6-Premise_LowDensity	8-Port_LA	1-Animal_HighDensity	2-Premise_HighDensity	3-Port_SF	4-SoutheastBorder
7-Animal_LowDensity	-0.2217	-0.0243	0.0460	0.5289	1.0226	1.0856	1.2378	2.9035
5-MarketStart	-0.0243	-0.2217	-0.1514	0.3315	0.8252	0.8882	1.0404	2.7061
6-Premise_LowDensity	0.0460	-0.1514	-0.2217	0.2612	0.7549	0.8179	0.9701	2.6358
8-Port_LA	0.5289	0.3315	0.2612	-0.2217	0.2720	0.3350	0.4872	2.1529
1-Animal_HighDensity	1.0226	0.8252	0.7549	0.2720	-0.2217	-0.1587	-0.0065	1.6593
2-Premise_HighDensity	1.0856	0.8882	0.8179	0.3350	-0.1587	-0.2217	-0.0695	1.5963
3-Port_SF	1.2378	1.0404	0.9701	0.4872	-0.0065	-0.0695	-0.2217	1.4441
4-SoutheastBorder	2.9035	2.7061	2.6358	2.1529	1.6593	1.5963	1.4441	-0.2217

Positive values show pairs of means that are significantly different.

Level		Mean
7-Animal_LowDensity	A	6.8468945
5-MarketStart	A B	6.6495313
6-Premise_LowDensity	B	6.5792188
8-Port_LA	C	6.0963281
1-Animal_HighDensity	D	5.6026563
2-Premise_HighDensity	D	5.5396484
3-Port_SF	D	5.3874609
4-SoutheastBorder	E	3.7217187

Levels not connected by same letter are significantly different.

Figure 16. Tukey-Kramer HSD comparison of means test for Detection Time. The graph shows the respective detection times output for each starting scenario. The green diamonds represent the mean detection time along with a 95% confidence interval. Generally, if the diamonds do not overlap, then the means are different. The statistical tests printed below the graph show which starting scenarios have statistically significant differences. The first matrix of values is Tukey's honestly significant difference (HSD) subtracted from the absolute difference between the means. In this case, the HSD is 0.2217, which is the value along the diagonal. Positive values show that the pairs of means are significantly different. The table displayed at the bottom of the figure is a sorted list of the means. The capital letters displayed in the middle of the table show which scenarios are within the HSD of another scenario. Scenarios not connected by the same letter are significantly different.



Means Comparisons

Comparisons for all pairs using Tukey-Kramer HSD

q*	Alpha
3.03247	0.05

Abs(Dif)-HSD

	1-Animal_HighDensity	2-Premise_HighDensity	3-Port_SF	4-SoutheastBorder	5-MarketStart	6-Premise_LowDensity	7-Animal_LowDensity	8-Port_LA
1-Animal_HighDensity	-235.5	448.5	532.4	914.8	960.0	1130.9	1173.7	1191.1
2-Premise_HighDensity	448.5	-235.5	-151.5	230.9	276.0	446.9	489.7	507.1
3-Port_SF	532.4	-151.5	-235.5	146.9	192.0	362.9	405.7	423.2
4-SoutheastBorder	914.8	230.9	146.9	-235.5	-190.4	-19.5	23.3	40.8
5-MarketStart	960.0	276.0	192.0	-190.4	-235.5	-64.6	-21.8	-4.3
6-Premise_LowDensity	1130.9	446.9	362.9	-19.5	-64.6	-235.5	-192.7	-175.3
7-Animal_LowDensity	1173.7	489.7	405.7	23.3	-21.8	-192.7	-235.5	-218.0
8-Port_LA	1191.1	507.1	423.2	40.8	-4.3	-175.3	-218.0	-235.5

Positive values show pairs of means that are significantly different.

Level		Mean
1-Animal_HighDensity	A	1465.7775
2-Premise_HighDensity	B	781.7919
3-Port_SF	B	697.8388
4-SoutheastBorder	C	315.4337
5-MarketStart	C D	270.3227
6-Premise_LowDensity	C D	99.3874
7-Animal_LowDensity	D	56.6070
8-Port_LA	D	39.1416

Levels not connected by same letter are significantly different.

Figure 17. Tukey-Kramer honestly significant difference (HSD) comparison of means test for Infected Premises. The graph shows the respective number of infected premises output for each starting scenario.

D. TIME UNTIL THE FIRST DETECTION OF AN INFECTED PREMISES

There is some debate within the literature about the importance of the length of time between when the first premises are infected and when the first premises are detected. Carpenter et al. (2011) use simulation to vary the length of time between when a facility is infected and when it is detected to estimate the economic impact of the outbreak to the United States and California, specifically. The authors find that the

shorter the time frame, the less expensive the outbreak. McLaws & Ribble (2007) research the relationship between outbreak size and early detection during outbreaks between 1992 and 2003. Given the authors compile their data from many countries with various ways of reporting, there is significant variability within the documented statistics. Their analysis of the statistics, however, leads them to conclude that there is no direct relationship between outbreak size and early detection. In this section, we will describe the distribution of the Detection Time mean, the relationship between infection and detection in our model, and then discuss a multiple-regression model and a partition tree model that explore the most important factors determining the detection time from our simulation.

1. Distribution of Detection Times

We begin by analyzing the distribution of the mean detection times across all factors and starting scenarios (see Figure 18). The mean is 5.8 days, with a standard deviation of 1.5 days, and the distribution is relatively normal in shape, although asymptotically bounded on the left at two days. The maximum mean detection time is 10.57 days.

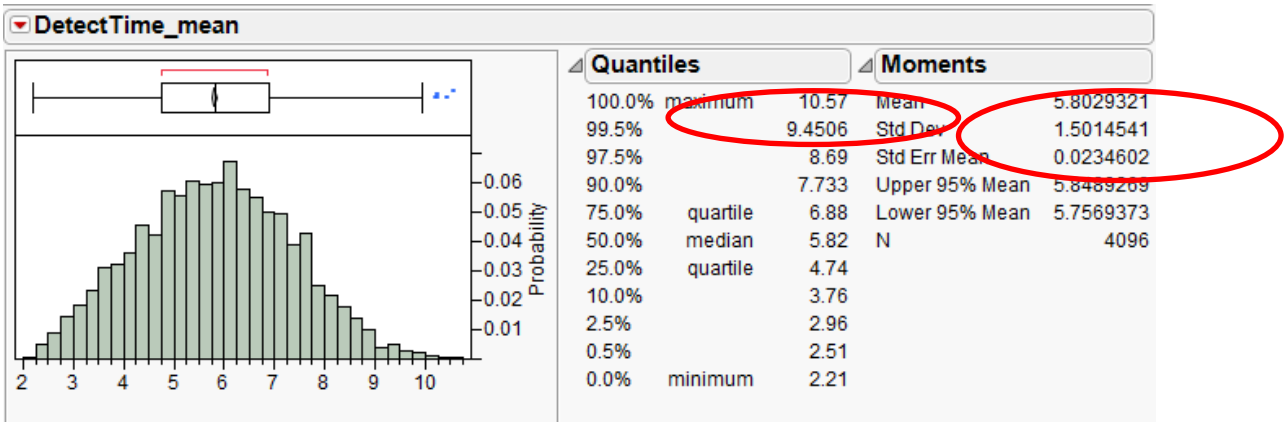


Figure 18. Distribution of Detection Time means across all factors and scenarios

2. Infection vs. Detection Results

The assumption that the shorter the length of time between infection and detection, then the smaller the number of infected premises did not hold for our simulation, in general. Instead, what we observe is that as the detection time increases,

the number of infected premises increases for a short amount of time and then decreases steadily (see Figure 19). This observation is also evident across design points with high or low potential for being large (see Figures 20 and 21). We discuss this perhaps counterintuitive result in Chapter VI.

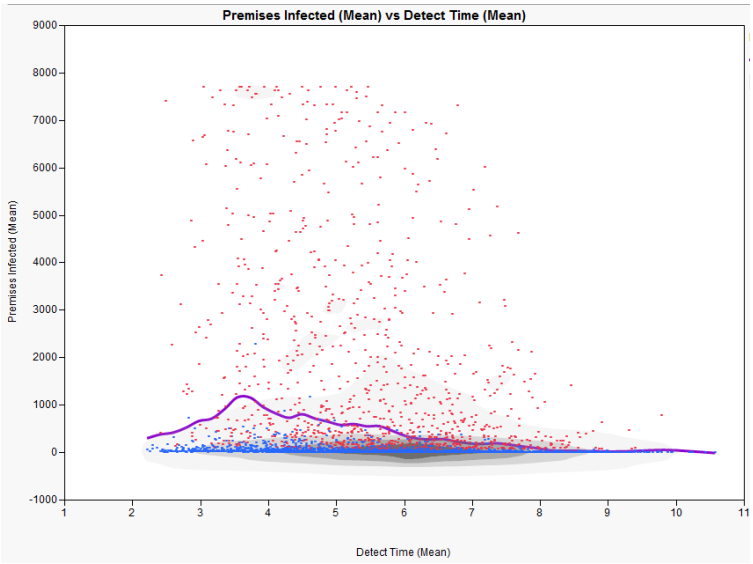


Figure 19. Average number of infected premises vs. average detection time. The smoother line shows the trend of the output, while the contours show the concentration of the data—the darker the area, the more data are located there. Red data points are those iterations of the simulation for which the data point has the potential to be large (over 7,700 premises), while blue data points are from design points that do not have this potential. Notice that as the average detection time increases, the number of infected premises also increases for a short time, then decreases steadily after about 3.7 days.

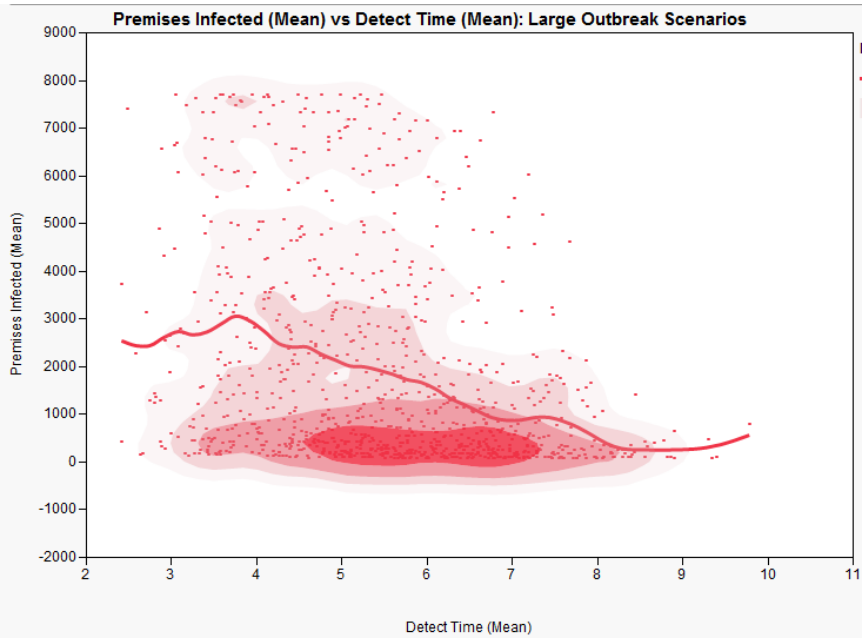


Figure 20. Average number of infected premises vs. average detection time for scenarios (design points) with the potential of a large outbreak. Notice the similar behavior in this figure and Figure 21.

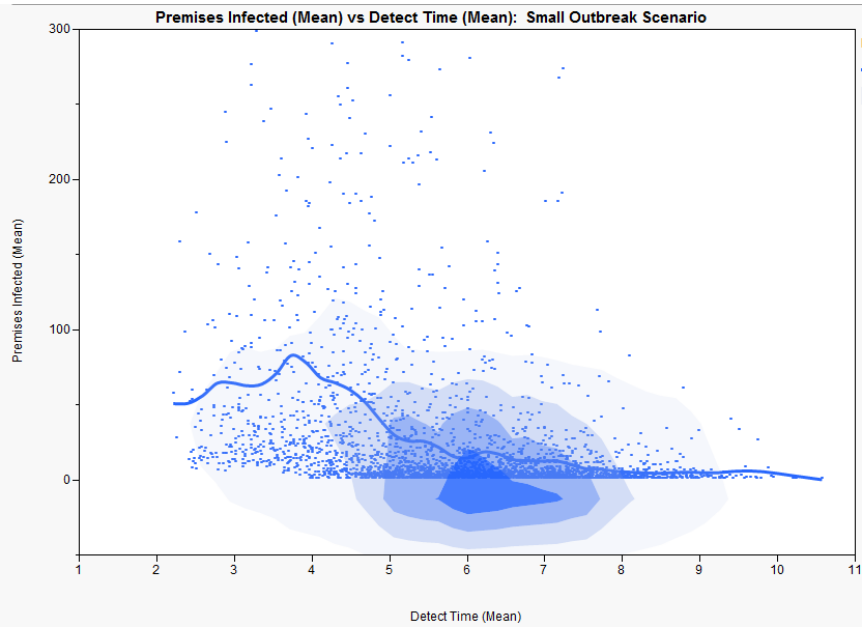


Figure 21. Average number of infected premises vs. average detection time for scenarios with low potential of a large outbreak.

3. Multiple-Regression Model

We use a forward Akaike Information Criterion (AIC) stepwise technique to create the multiple-regression model. This technique uses an algorithm to add significant factors to the model, while penalizing the addition of insignificant factors or those with insignificant coefficients and works well with large datasets (Posada & Buckley, 2004). We allow the algorithm to search through all noise and decision factor main effects and second order polynomials to develop a model. The fitted model contains 14 terms that explain about 42% of the variability in the data and produces an adjusted R^2 of 0.417 (see Figure 22).

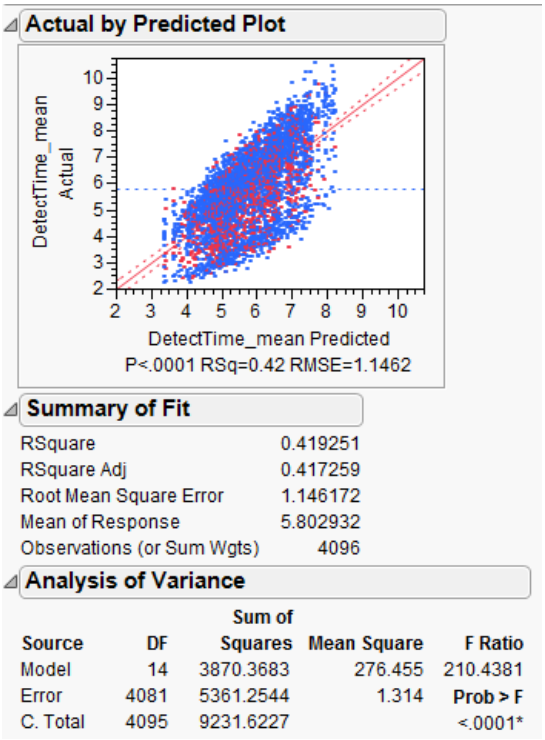


Figure 22. Fitted model for Detect Time mean. Adjusted R^2 is 0.417. Actual vs. Predicted responses are plotted and an Analysis of Variance (ANOVA) is shown indicating that the model is significant, with a p-value of < 0.0001. The "Prob>F" statistic shows the p-value of the test. Since the p-value is smaller than 0.05, we reject the null hypothesis that the factors included in the regression have no effect on the response variable.

We must now check the adequacy of the model based on the four assumptions, of which the model passes two. Independence is satisfied because all iterations and all

design points were randomly chosen, and the residual mean is zero, as shown in Figure 23. However, the residuals do not display constant variance (see Figure 23), nor are they normally distributed (see Figure 24).

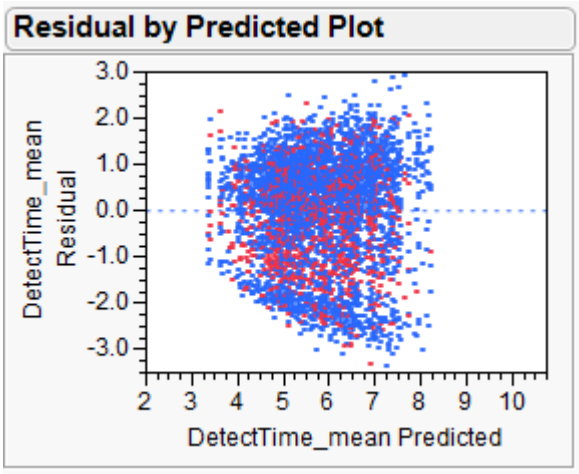


Figure 23. Residual by Predicted plot of multiple-regression model of the Detect Time mean. The mean of the residuals is 0, identified by the blue dashed line; however, the residuals display heteroscedasticity.

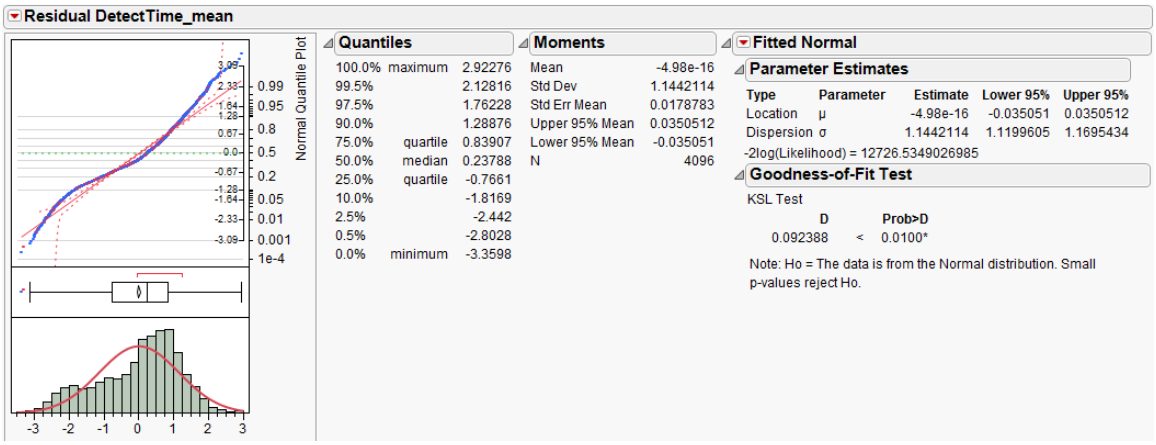


Figure 24. Distribution of the residual errors of the multiple-regression model of the Detect Time mean. We fit the distribution to a normal curve in the right column of the figure. Using the mean and standard deviation of the residuals, shown in the "Moments" column, JMP builds a fitted normal distribution. We then perform a Kolmogorov-Smirnov-Lillefors (KSL) Test for goodness of fit between the distribution of the residuals and the fitted normal distribution. The "Prob>D" statistic shows the p-value of the test. Since the p-value is smaller than 0.05, we reject the null hypothesis that the distribution of residuals is normal.

We attempt to correct the heteroscedasticity of the residuals by performing a transformation on the Detect Time and rerunning the forward AIC stepwise algorithm. We select a transformation to correct the nonconstant variance and nonnormality by trying several usual transformations including the log, square root, and exponential (Montgomery, Peck, & Vining, 2006). Ultimately, we choose the square root transformation because it best corrects the problems. The resulting fitted model has a lower adjusted R^2 of 0.402 (see Figure 25), but now passes the constant variance assumption (see Figure 26). However, we were unable to meet the assumption of the residuals being normally distributed (see Figure 27).

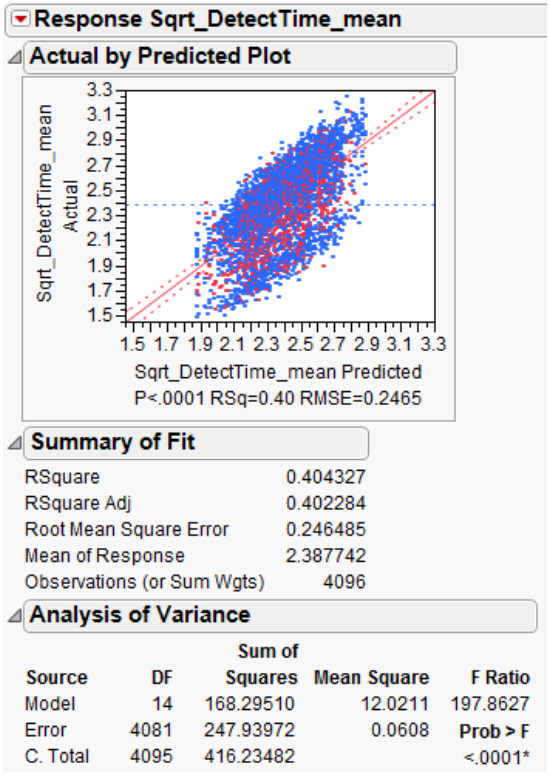


Figure 25. Fitted model for Square Root of Detect Time mean. Adjusted R^2 is 0.402. Actual vs. Predicted responses are plotted and an Analysis of Variance (ANOVA) is shown indicating that the model is significant, with a p-value of < 0.0001.

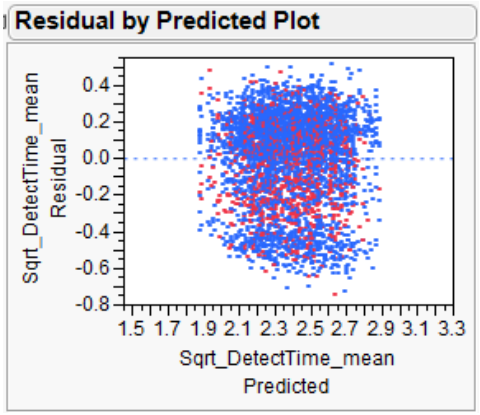


Figure 26. Residual by Predicted plot of the multiple-regression model of the Square Root of Detect Time mean. The mean of the residuals is 0, identified by the blue dashed line, and we have removed the heteroscedasticity.

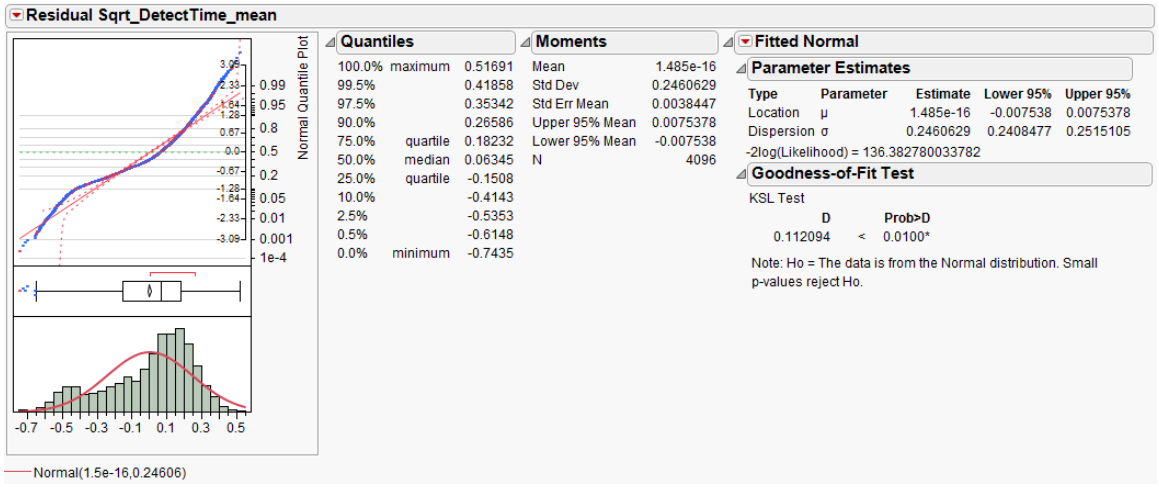


Figure 27. Distribution of the residual errors of the multiple-regression model of the Square Root of Detect Time mean. We fit the distribution to a normal curve and perform a KSL Test for goodness of fit, which the distribution fails.

Even though our model violates the normality of residuals assumption, we present it regardless. The factors within the model sorted by significance are presented in Figure 28. Dairy surveillance parameters, especially the amount of delay between when a certain premises is inspected and when it is determined to be infected (DelayToDetection), are the most significant factors. These three parameters all have

positive coefficients, which means that as they increase, so does the DetectTime mean. The LocalSpreadMultiplier, in contrast, has a negative coefficient. So, as the local spread is allowed to spread longer distances, the detection time decreases.

Response Sqrt_DetectTime_mean

Sorted Parameter Estimates

Term	Estimate	Std Error	t Ratio	Prob>|t|
Surveillance3.DelayToDetection.GeneralSurv_Dairy_before	0.1430387	0.003337	42.86	<.0001*
Surveillance3.VisitDelay.GeneralSurv_Dairy_before	0.1068051	0.005333	20.03	<.0001*
Surveillance3.VisitFrequency.GeneralSurv_Dairy_before	0.0632422	0.005339	11.84	<.0001*
LocalSpread1.Multiplier	-0.077988	0.007611	-10.25	<.0001*
Surveillance1.VisitDelay.GenSurv	0.0162105	0.001665	9.74	<.0001*
Surveillance1.DelayToDetection.GenSurv	0.0179894	0.002667	6.74	<.0001*
Infectivity1.TimeToClinicalSigns	-0.010811	0.001903	-5.68	<.0001*
AllFarms.ProbabilityOfTransmission	-0.188327	0.033299	-5.66	<.0001*
(Infectivity1.TimeToClinicalSigns-4.5)*(Infectivity1.TimeToClinicalSigns-4.5)	0.0048473	0.001065	4.55	<.0001*
AllMovements.MovementDistance	-0.027892	0.007613	-3.66	0.0003*
MovementType15.NumberPerTimePeriod.24.34.114.214.314.310.211.213.51.61.53.63.121.131.151.161.	-0.113242	0.043879	-2.58	0.0099*
MovementType10.NumberPerTimePeriod.121.131.151.161.	-0.136201	0.054169	-2.51	0.0120*
(Surveillance1.VisitDelay.GenSurv-6)*(Surveillance1.VisitDelay.GenSurv-6)	-0.001412	0.000814	-1.73	0.0829
Surveillance3.DetectionProbability.....GeneralSurv_Dairy_before	0.0388201	0.027223	1.43	0.1540

Figure 28. Sorted Parameter Estimates of the Square Root of Detect Time mean model. The "Term" column lists the factors used in the model. The "Estimate" is the parameter estimate for the linear model, and the "Std Error" is the standard error of the parameter estimate. The "t-Ratio" is the ratio of the parameter estimate to the standard error and is used as the test statistic when testing the factor's importance to the model. The horizontal bars graphically show the relative t-ratio of each factor in relation to the most important factor, while the Prob>|t| shows the probability of obtaining a t-ratio greater than the factor t-ratio at random. This is called the p-value. Overall, this figure shows the relative importance of the surveillance procedures at dairies to the mean detection time of the first detected premises. Appendix A describes the parameters modeled in detail.

4. Partition Tree Model

We now compare our multiple-regression model to a partition tree. As described earlier, the partition tree splits the factors sequentially in order to maximize the difference in the mean of continuous factors, or the probability of categorical factors, so that the nodes, or leaves, are as much alike as possible. We choose to split the factors a total of 27 times in order to achieve an R^2 of 0.39; a similar explanation of the variance as the multiple-regression model. The three most significant factors in the partition tree model are identical to the multiple-regression model, and include the three parameters describing the surveillance operations on dairy premises. The first split in the model is

on the amount of delay between when premises are inspected and when they are determined to be infected (DelayToDetection). The optimal split point is at 3.411. This means that the average Detect Time of those design points tested in the model, which have DelayToDetection parameter settings of less than 3.411 days, are most different from those with settings above 3.411 days. In this case, the mean Detect Time of those design points with the DelayToDetection setting below 3.411 is 5.23 days, and the mean of those design points above 3.411 is 6.67 days. We display the contributions of the significant parameters in Figure 29.

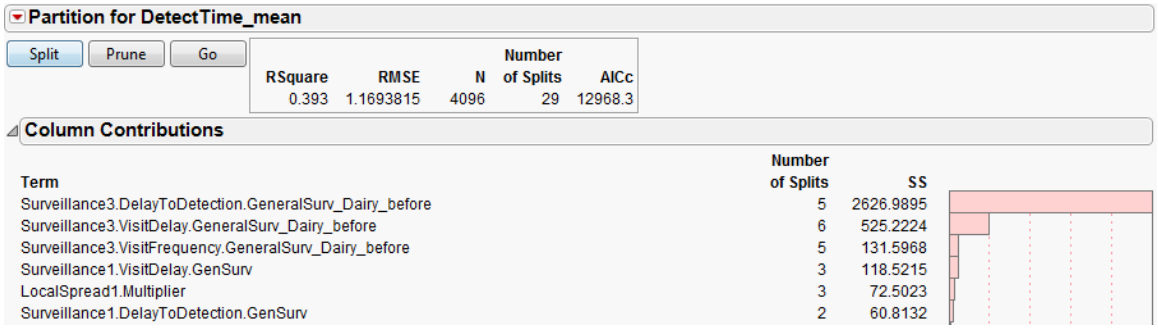


Figure 29. Partition Tree model for Detect Time mean. The "Term" column shows the most significant factors affecting the mean detection time. Here, those factors are the surveillance operations on dairy premises. The "Number of Splits" column shows how many times the partition tree was split on a factor. The "SS" column shows the sum, over the multiple splits, of the squared differences between the two leaves into which the factor was split. Larger numbers show a larger distance between the means of the leaves. The horizontal bars simply show the relative contribution of the factors in terms of the first factor displayed. For example, 525.2224 is approximately 20% of 2626.9895. Therefore, the second bar is approximately 20% of the size of the first bar.

E. MEAN NUMBER OF INFECTED PREMISES

As discussed in Section A, the correlations between the MOEs we use are high. So, here we show the models developed for the mean number of infected premises as a proxy for the other MOE. We first describe a multiple-regression model, followed by a partition tree.

1. Distribution of Infected Premises

We begin by analyzing the distribution of the mean Infected Premises across all factors and starting scenarios (see Figure 30). The mean is 466 premises, with a standard deviation of 1,324 premises, and the distribution is extremely right skewed. The maximum mean number of infected premises is 7,700, which was the maximum we set in the control file of the simulation. We explore this upper bound further in Section F.

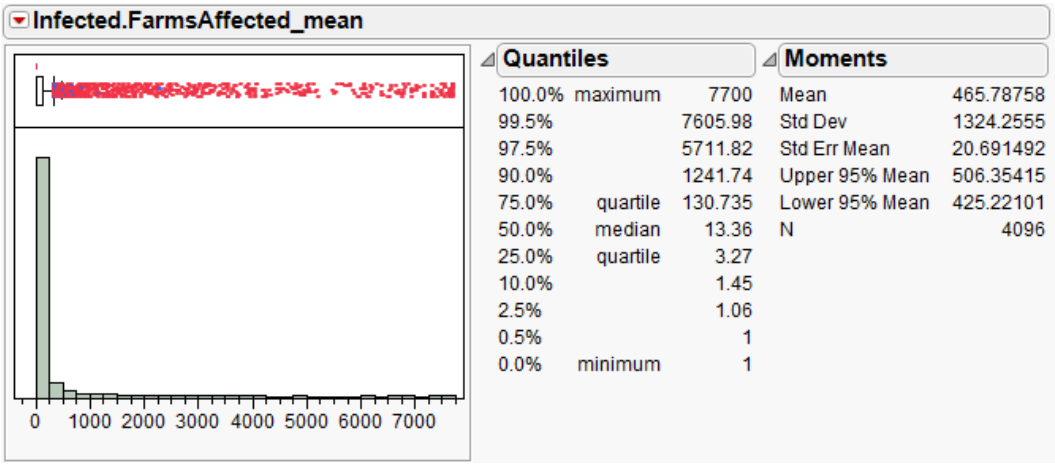


Figure 30. Distribution of Infected Premises means across all factors and scenarios

2. Multiple-Regression Model

As we did in our analysis of Detection Time, we use a forward AIC stepwise technique to create the multiple-regression model. We allow the algorithm to search through all noise and decision factor main effects and second order polynomials to develop a model. The fitted model contains 52 terms that explain about 21% of the variability in the data and produces an adjusted R^2 of 0.213 (see Figure 31).

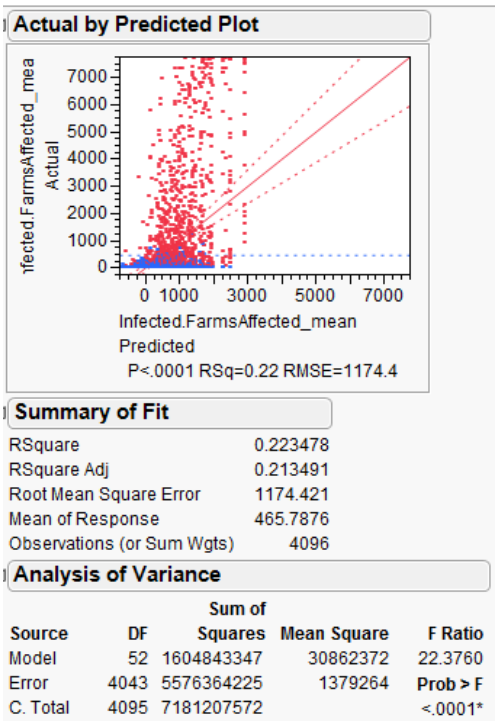


Figure 31. Fitted model for Infected Premises mean. Adjusted R^2 is 0.213. Actual vs. Predicted responses are plotted and an Analysis of Variance (ANOVA) is shown, indicating that the model is significant, with a p-value of < 0.0001.

We now check the adequacy of the model based on the four assumptions, of which the model passes two. Independence is satisfied because all iterations and all design points were randomly chosen, and the residual mean is zero, as shown in Figure 32. However, the residuals do not display constant variance (see Figure 32), nor are they normally distributed (see Figure 33).

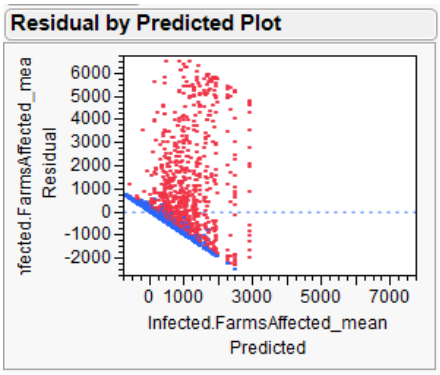


Figure 32. Residual by Predicted plot of a multiple -egression model of the mean number of Infected Premises. The mean of the residuals is 0, identified by the blue dashed line. We have removed the heteroscedasticity.

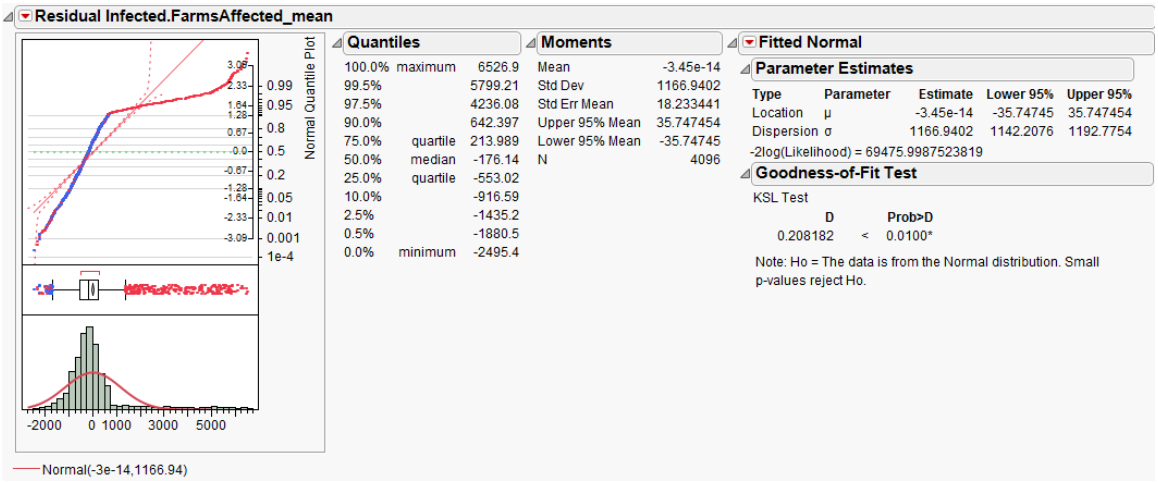


Figure 33. Distribution of the residual errors of the multiple-regression model of the mean number of Infected Premises. We fit the distribution to a normal curve and perform a KSL Test for goodness of fit, which the distribution fails.

In order to address the constant variance and normality assumptions, we again attempt to transform the response variable with one of several methods described in Section D.3. The usual transformations do not correct the problems, however, so we apply a Box-Cox transformation of the Infected Premises mean. Box and Cox (1964) use a method of maximum likelihood to estimate a power to be applied to the response variable in order to correct these problems. The resulting model contains 35 terms and

has an adjusted R^2 of 0.323 (see Figure 34). The transformation corrects the heteroscedasticity (see Figure 35) and the residuals appear normal, even though they fail the goodness of fit test (see Figure 36).

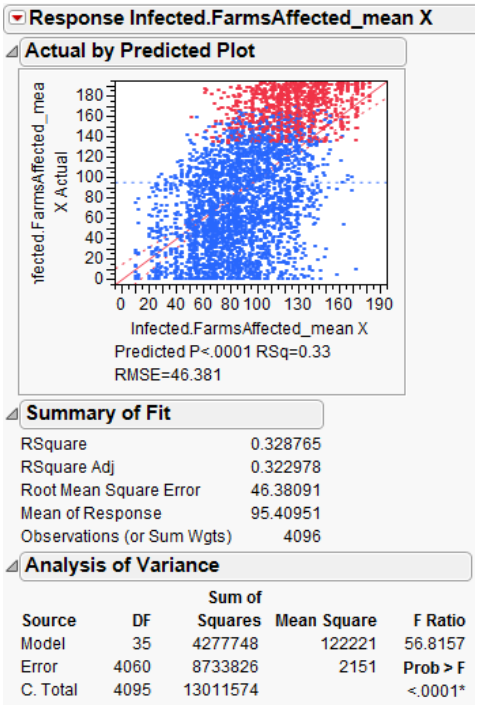


Figure 34. Fitted model for Box-Cox transformed Infected Premises mean. Adjusted R^2 is 0.323. Actual vs. Predicted responses are plotted and an Analysis of Variance (ANOVA) is shown indicating that the model is significant with a p-value of < 0.0001.

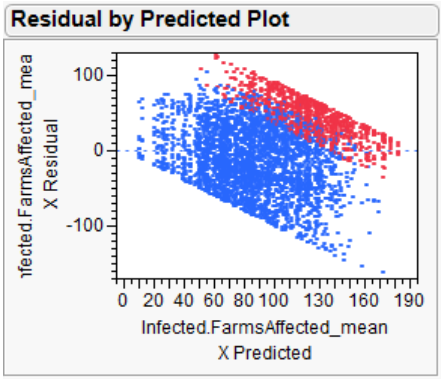


Figure 35. Residual by Predicted plot of multiple regression model of the Box-Cox transformed mean number of Infected Premises. The mean of the residuals is 0, identified by the blue dashed line. We have removed the heteroscedasticity.

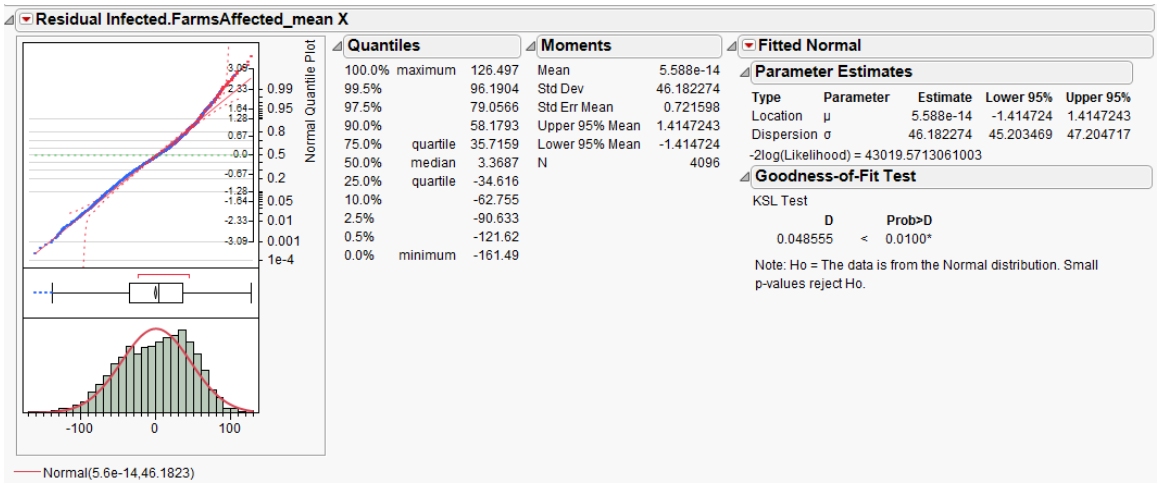


Figure 36. Distribution of the residual errors of the multiple-regression model of the Box-Cox transformed mean number of Infected Premises. We fit the distribution to a normal curve and perform a KSL Test for goodness of fit, which the distribution fails, even though the plots look fairly normal

The factors within the model sorted by significance are presented in Figure 37. The four most significant factors to this model are all noise factors including the local spread, the probability of transmission, the overall movement distances, and some indirect movement types. The most significant decision factors include the surveillance procedures at dairies, the size of the surveillance zone, the number of resources available to depopulate, and the length of time between the first detection and when the full amount of depopulation resources are available.

Sorted Parameter Estimates

Term	Estimate	Std Error	t Ratio	Prob>|t|
LocalSpread1.Multiplier	42.816222	1.442194	29.69	<.0001*
AllFarms.ProbabilityOfTransmission	113.55217	6.344606	17.90	<.0001*
AllMovements.MovementDistance	25.036147	1.450991	17.25	<.0001*
MovementType15.NumberPerTimePeriod.24.34.114.214.314.310.211.213.51.61.53.63.121.131.151.161.	69.999722	8.252575	8.48	<.0001*
Surveillance3.DelayToDetection.GeneralSurv_Dairy_before	5.3426831	0.63531	8.41	<.0001*
Zone4.OutsideRadius1.SurvZone	-0.000344	0.000051	-6.74	<.0001*
Resource1.TimePeriodStart2.FullUtilization	0.8824141	0.132561	6.66	<.0001*
Resource1.PerTimePeriod	-8.55457	1.688138	-5.07	<.0001*
Surveillance7.DelayToDetection.Trace	2.2849799	0.634006	3.60	0.0003*
Surveillance3.VisitFrequency.GeneralSurv_Dairy_before	3.702636	1.034681	3.58	0.0003*
AllMarketsClosed[False]	2.5836872	0.732239	3.53	0.0004*
MovementType10.NumberPerTimePeriod.121.131.151.161.	34.858459	10.32757	3.38	0.0007*
Surveillance3.VisitDelay.GeneralSurv_Dairy_before	3.1662103	1.007438	3.14	0.0017*
Surveillance7.VisitFrequency.Trace	1.1313069	0.423136	2.67	0.0075*
Surveillance4.VisitDelay.GeneralSurv_Dairy_after	4.3126067	1.682212	2.56	0.0104*
Surveillance1.DelayToDetection.GenSurv	1.1924767	0.50436	2.36	0.0181*
(Resource1.PerTimePeriod-1.25)*(Resource1.PerTimePeriod-1.25)	10.708535	4.584412	2.34	0.0195*
Surveillance5.DetectionProbability.....ControlArea	-29.62815	13.24673	-2.24	0.0254*
(AllMovements.MovementDistance-1.125)*(AllMovements.MovementDistance-1.125)	-7.395295	3.35949	-2.20	0.0278*
(Surveillance6.DetectionProbability.....sheep..SurvZone-0.825)*(Surveillance6.DetectionProbability.....sheep..SurvZone-0.825)	-358.0525	162.9751	-2.20	0.0281*
AllMarkets.ProbabilityOfTransmission	10.95294	5.07505	2.16	0.0310*
(Surveillance6.DelayToDetection.SurvZone-1.5)*(Surveillance6.DelayToDetection.SurvZone-1.5)	-21.7429	10.12433	-2.15	0.0318*
(Surveillance2.VisitFrequency.GeneralAfterFirstDetection-4.5)*(Surveillance2.VisitFrequency.GeneralAfterFirstDetection-4.5)	-0.798958	0.405354	-1.97	0.0488*

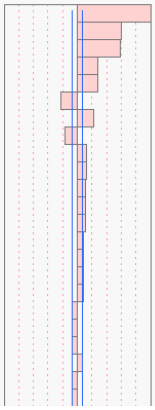


Figure 37. Sorted Parameter Estimates of the Box-Cox transformed mean number of Infected Premises model. This shows that noise factors including the local spread, the probability of transmission, the overall movement distances, and some indirect movement types, are the most significant factors to the mean number of infected premises. The most significant decision factors include the surveillance procedures at dairies, the size of the surveillance zone, the number of resources available to depopulate, and the length of time between the first detection and when the full amount of depopulation resources are available. Appendix A describes the parameters modeled in detail.

3. Partition Tree Model

We again compare our multiple-regression model to a partition tree. We choose to split the factors a total of 50 times in order to achieve an R^2 of 0.31; a similar explanation of the variance as the multiple-regression model (see Figure 38). The noise factors are still prevalent within the model, with the Local Spread Multiplier as the first split. It splits at 1.5788, which is equivalent to stating that the distance bands for this parameter are increased from the base case of 1,000 m, 2,000 m, and 3,000 m to 1,578 m, 3,157 m, and 4,736 m, respectively. Interestingly, the parameter describing the total capacity to depopulate animals is the second split. It splits for those observations with a Local Spread Multiplier of greater than 1.5788 at 0.638. This is equivalent to having resources to depopulate 12,760 animals per day. The detection probability for sheep in the surveillance zone is a factor that is not significant in any of the models up to this point, but is in this model.

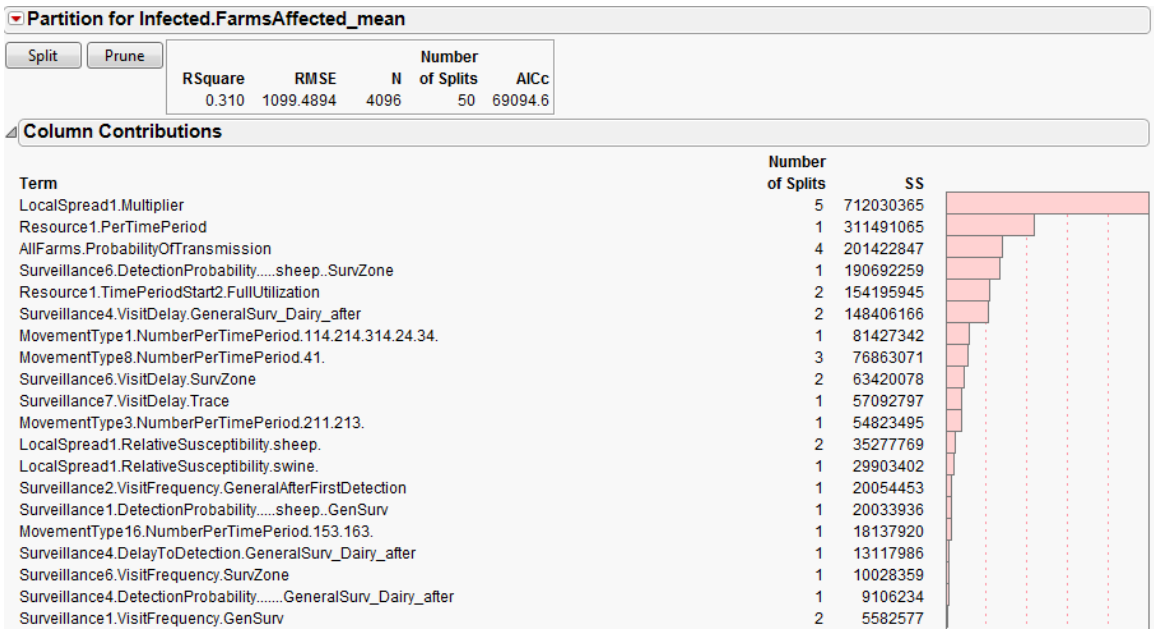


Figure 38. Partition Tree model for Infected Premises mean. The most significant noise factors affecting the mean number of infected premises are the Local Spread Multiplier, the premises probability of transmission, and the detection probability of infected sheep in the surveillance zone. The most significant decision factors are the number of resources available to depopulate, the amount of ramp-up time until all depopulation resources are available, and the amount of delay between surveillance visits at likeDairy premises after the first infected premises of the outbreak is detected.

F. MODELS TO EXPLORE THE POTENTIAL FOR A LARGE OUTBREAK

One concern we have with the multiple-regression and partition tree models for the mean number of Infected Premises is that we set a maximum number of this MOE within the simulation. Because of this, we feel that the model may be underestimating the mean over all simulation iterations since outbreaks were stopped once the number of infected premises reached 7,700. Therefore, we present a new MOE describing the percentage of times a design point reached 7,700 infected premises. This MOE can be thought of as a surrogate for whether the design point has *the potential* to be a large outbreak. In this section, we describe the results obtained with the new MOE using a multiple-regression model and with a partition tree.

1. Multiple-Regression Model

We add another column to our data with the frequency that the design point reached the maximum number of infected premises out of the 100 iterations, and use this new column as the response variable in a multiple-regression model. We exclude five out of the seven starting scenarios because they rarely reach the maximum infected premises limit and focus on those that do. The starting scenarios modeled using this MOE are the High Animal Density, High Premises Density, and Port of San Francisco scenarios. Again, we use a forward AIC stepwise technique, and allow the algorithm to search through all noise and decision factor main effects, two-way interactions, and second order polynomials to develop a model. The fitted model contains 45 terms, which produces an adjusted R^2 of 0.402 (see Figure 39).

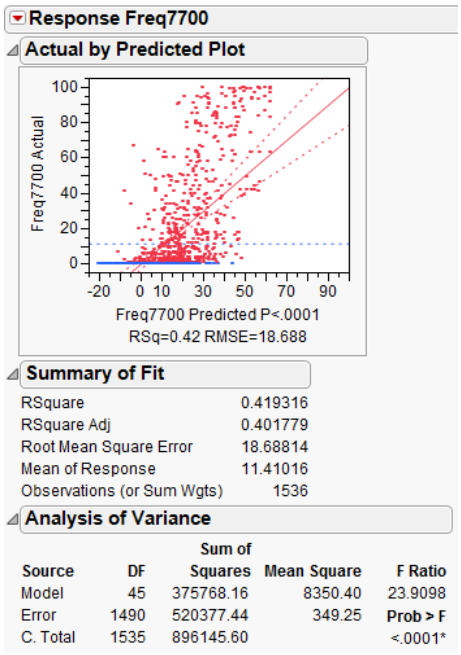


Figure 39. Fitted model for Frequency Iterations with the Maximum Number of Infected Premises. Adjusted R^2 is 0.402. Actual vs. Predicted responses are plotted and an Analysis of Variance (ANOVA) is shown indicating that the model is significant, with a p-value of < 0.0001.

We again check the adequacy of the model based on the four assumptions, of which the model passes two. Independence is satisfied because all iterations and all design points were randomly chosen, and the residual mean is zero. However, the

residuals do not display constant variance, nor are they normally distributed. Again, we attempt to transform the MOE using the usual methods, and ultimately use a log transformation to obtain the model shown in Figure 40. The resulting model includes 45 terms and produces an adjusted R^2 of 0.50. The transformed model now displays constant variance and the residuals appear normal, even though they fail the goodness of fit test (see Figures 41 and 42).

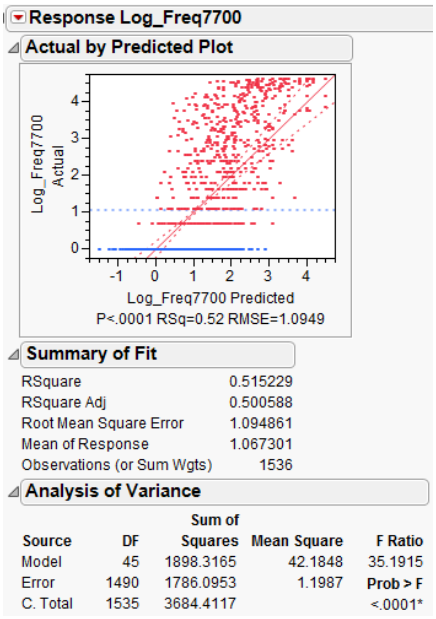


Figure 40. Fitted model for the Log of Frequency Iterations with the Maximum Number of Infected Premises. Adjusted R^2 is 0.50. Actual vs. Predicted responses are plotted and an Analysis of Variance (ANOVA) is shown indicating that the model is significant with a p-value of < 0.0001.

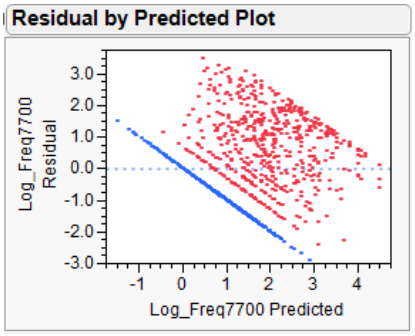


Figure 41. Residual by Predicted plot of the multiple-regression model of the log transformed Frequency of Iterations with the Maximum Number of Infected Premises. The mean of the residuals is 0, identified by the blue dashed line. We have removed the heteroscedasticity.

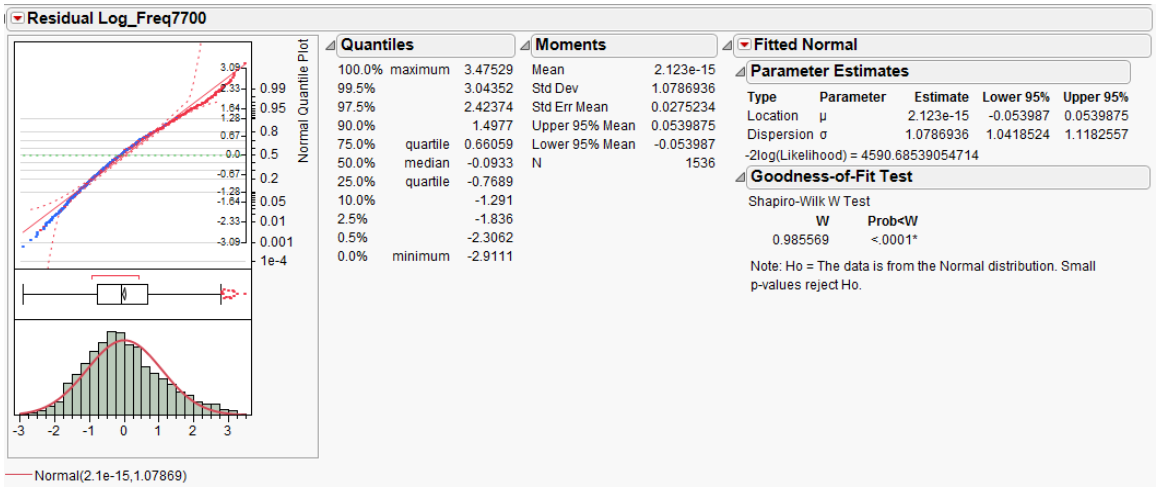


Figure 42. Distribution of the residual errors of the multiple-regression model log transformed Frequency of Iterations with the Maximum Number of Infected Premises. We fit the distribution to a normal curve and perform a Shapiro-Wilk W Test for goodness of fit, which JMP uses when the number of data points is less than 2,000. The distribution fails even though the plots appear fairly normal.

The factors within the model sorted by significance are presented in Figure 43. The two most significant factors to this model—the local spread multiplier and the farm probability of transmission—remain the same as for the infected premises MOE discussed in Section E. However, the next two most significant factors are now the decision factors depopulation resources available per day and the amount of ramp-up time until all depopulation resources are available. The other significant factors are similar to those in the model for the infected premises MOE.

Response Log_Freq7700

Sorted Parameter Estimates

Term	Estimate	Std Error	t Ratio	Prob>|t|
LocalSpread1.Multiplier	1.4419663	0.055842	25.82	<.0001*
AllFarms.ProbabilityOfTransmission	3.554424	0.243638	14.59	<.0001*
Resource1.TimePeriodStart2.FullUtilization	0.0741479	0.005146	14.41	<.0001*
Resource1.PerTimePeriod	-0.652056	0.065109	-10.01	<.0001*
AllMovements.MovementDistance	0.4003581	0.056059	7.14	<.0001*
(LocalSpread1.Multiplier-1.125)*(LocalSpread1.Multiplier-1.125)	0.8009769	0.127297	6.29	<.0001*
Zone4.OutsideRadius1.SurvZone	-9.522e-6	0.000002	-4.74	<.0001*
(Resource1.PerTimePeriod-1.25)*(Resource1.PerTimePeriod-1.25)	0.7641753	0.180578	4.23	<.0001*
Surveillance3.DelayToDetection.GeneralSurv_Dairy_before	0.1030071	0.024488	4.21	<.0001*
Surveillance1.DelayToDetection.GenSurv	0.0725872	0.019719	3.68	0.0002*
MovementType15.NumberPerTimePeriod.24.34.114.214.314.310.211.213.51.61.53.63.121.131.151.161.	1.0174205	0.321961	3.16	0.0016*
(Surveillance4.VisitDelay.GeneralSurv_Dairy_after-1.25)*(Surveillance4.VisitDelay.GeneralSurv_Dairy_after-1.25)	0.541636	0.175609	3.08	0.0021*
AllMarkets.ProbabilityOfTransmission	0.574172	0.195975	2.93	0.0034*
(MovementType17.NumberPerTimePeriod.31.32.43.73.-1.02217)*(MovementType17.NumberPerTimePeriod.31.32.43.73.-1.02217)	-0.255746	0.093377	-2.74	0.0062*
(AllMovements.MovementDistance-1.125)*(AllMovements.MovementDistance-1.125)	-0.337962	0.130049	-2.60	0.0094*
Zone2.OutsideRadius1.ControlArea	-1.267e-5	4.884e-6	-2.59	0.0096*
(Surveillance1.DelayToDetection.GenSurv-4.5)*(Surveillance1.DelayToDetection.GenSurv-4.5)	-0.040259	0.015831	-2.54	0.0111*
(MovementType7.NumberPerTimePeriod.33.-0.54667)*(MovementType7.NumberPerTimePeriod.33.-0.54667)	11.133826	4.396951	2.53	0.0114*
AllMarketsClosed[False]	0.0702201	0.028316	2.48	0.0133*
Surveillance1.DetectionProbability.....GenSurv	-0.244543	0.099596	-2.46	0.0142*
Surveillance3.VisitFrequency.GeneralSurv_Dairy_before	0.094896	0.040284	2.36	0.0186*
(Tracing1.ProbMovementForgotten....-0.425)*(Tracing1.ProbMovementForgotten....-0.425)	1.5354021	0.697771	2.20	0.0279*
LocalSpread1.RelativeSusceptibility.swine.	2.1655493	0.99146	2.18	0.0291*
(Surveillance2.VisitFrequency.GeneralAfterFirstDetection-4.5)*(Surveillance2.VisitFrequency.GeneralAfterFirstDetection-4.5)	-0.034451	0.015897	-2.17	0.0304*
Surveillance3.DetectionProbability.....GeneralSurv_Dairy_before	-0.420572	0.200575	-2.10	0.0362*
Surveillance7.DelayToDetection.Trace	0.0496163	0.024379	2.04	0.0420*
(Surveillance1.VisitFrequency.GenSurv-6.5)*(Surveillance1.VisitFrequency.GenSurv-6.5)	0.0160833	0.008186	1.96	0.0496*

Figure 43. Sorted Parameter Estimates of the log transformed Frequency of Iterations with the Maximum Number of Infected Premises model. This shows that noise factors, including the local spread, the probability of transmission, the overall movement distances, and some indirect movement types, are the most significant factors to the model. The most significant decision factors include the number of resources available to depopulate, the length of time between the first detection and when the full amount of depopulation resources are available, the surveillance procedures at dairies, and the size of the surveillance zone.

2. Partition Tree Model

We again compare our multiple-regression model to a partition tree. We choose to split the factors a total of 20 times in order to achieve an R^2 of 0.52, a similar explanation of the variance as the multiple regression model (see Figure 44). The noise factors are still prevalent within the model, with the Local Spread Multiplier as the first split. It splits at 1.5788, which is identical to the first split of the mean of Infected Premises partition tree. The next split is on the length of time between the first detection and when the full amount of depopulation resources is available. It splits for those observations with a Local Spread Multiplier of greater than 1.5788 at nine days. The means of the two leaves created by this split are 10.49 for outbreaks, where the resources are available before 9 days, and 39.85 days for those greater than or equal to 9 days. This is like saying that for those outbreaks whose local spread can reach distances of

approximately 4,700 m, having the full number of depopulation resources within nine days will, on average, reduce the number of times the model will reach 7,700 premises infected from 39.85 times to 10.49 times out of 100 iterations.

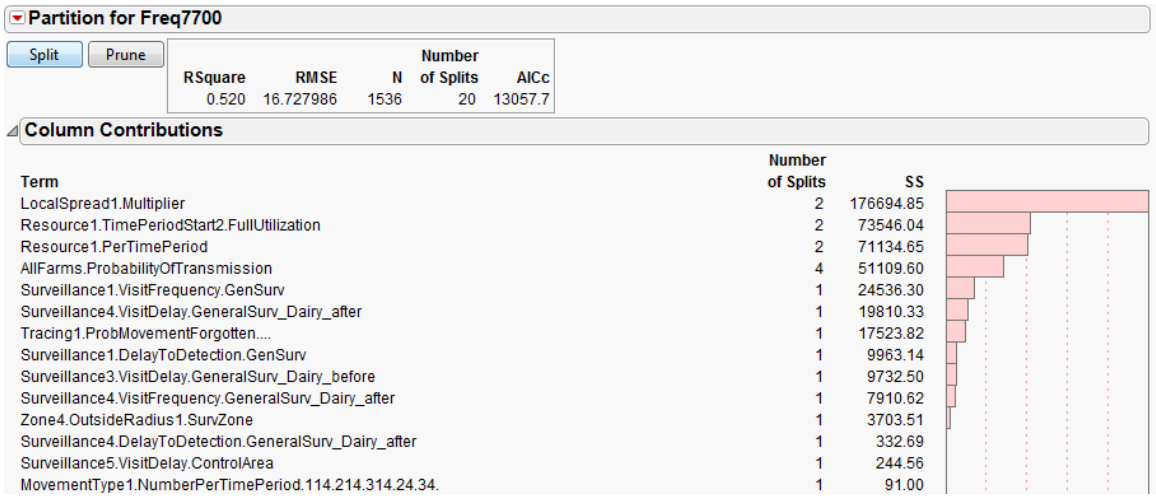


Figure 44. Partition Tree model for Infected Premises mean. The most significant noise factors affecting the mean number of infected premises are the Local Spread Multiplier and the farm probability of transmission. The most significant decision factors are the amount of ramp-up time until all depopulation resources are available, the number of resources available to depopulate, the general surveillance frequency of all non-dairy-like premises prior to the first premises of the outbreak is detected, and the amount of delay between surveillance visits at likeDairy premises after the first infected premises of the outbreak is detected.

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VI. CONCLUSIONS

The results of Chapter V should not be interpreted as individual predictions on outbreak scenarios. Instead, we vary the model 400,000 times to attempt to indicate which parameters are the most important when modeling an outbreak in a modern, state-of-the-art simulator, ISP. In Chapter I, we pose four research questions in order to focus our analysis. Based on the results in Chapter V, we address those initial research questions as well as discuss a surprising finding about depopulation resources. We organize the sections of this chapter in the following manner:

- **Disease Spread Parameters:** Which disease spread parameters are most important to the simulation of an outbreak of FMD in California?
- **Control Area and Surveillance Zone Sizes:** In response to a variety of outbreak scenarios, what are the optimal sizes of Control Areas and Surveillance Zones that efficiently eradicate the disease and also minimize the economic impact to the livestock industry?
- **Surveillance Procedures:** How often should livestock facilities be screened for FMD prior to and during an outbreak?
- **Starting Scenarios:** Of the outbreak scenarios modeled in this thesis, which are the most dangerous for California?
- **Depopulation Resources:** How do the availability and number of depopulation resources affect the spread of FMD in California?

A. DISEASE-SPREAD PARAMETERS

Several disease parameters affect all of the models we develop. The three that seem most significant to our models are: the Local Spread Multiplier, the All Movements Distance Multiplier, and the Farm Probability of Transmission. Below, we discuss these disease-spread parameters, as well as a parameter we expected to be more significant—the movements between farms and markets.

1. The Local Spread Multiplier is a significant factor in all of the regressions and all of the partition trees. Its effect on the mean detection time is negative,

meaning that as the local spread is allowed to move farther away from the infected premises, the mean detection time decreases. This is probably because the farther the virus moves, the more premises it comes in contact with. This leads to more premises being infected and increases the all of the surveillance factors probabilities to detect the disease.

The Local Spread Multiplier also has a significant effect on the size of the outbreaks, measured both by mean number of infected premises and by the frequency of iterations reaching 7,700 infected premises. Both MOE partition trees split first on the Local Spread Multiplier and they split at the same point. This suggests that there may be either an issue with the simulator at this distance of spread or that when the randomized premises were located during the development of the data, this distance was significant in the calculation. Whether or not this distance is truly significant is difficult to determine since the locations of the premises are not exact. The local spread parameter serves as a "catch all" parameter describing the spread of the disease when we are unable to determine a reason for a premises to be infected other than its proximity to another infected premises. So, as we begin to understand more about how the virus spreads, the impact of the local spread parameter will likely be decreased because infections will be able to be attributed to other causes.

2. The All Movements Distance Multiplier

The all Movements Distance Multiplier is significant in all of the regression models, but is not significant in any of the partition trees. This parameter is similar to the Local Spread Multiplier in that it controls how far movements of infected animals can travel, but it is different in that movements only occur at specific rates. So, its effect on how many other premises are infected is less direct than the local spread parameter. By being able to move greater distances, this parameter increases the chances that the virus will spread to a geographic area outside of the effect of local spread, or beyond the effect of implemented control measures. This increases the probability that certain premises are infected even though they at a lower risk from local spread or in locations outside of

restricted areas. The other significant characteristic of this parameter is that its effect is greatly diminished once the first detection of infected premises is made and movement restrictions are put in place.

3. The Farm Probability of Transmission

The Farm Probability of Transmission is significant in all of the models, which is not surprising. The higher the probability of transmission is, the larger the outbreak is, and the shorter the detection time is—since there is more disease to find. The fact that this parameter shows up in all of our models is more of a confirmation that the simulation is running correctly than an insight into the disease spread.

4. Market Movement Type 12

Market Movement Type 12 was not a factor in any of our models. This was likely because the experimental design did not sufficiently vary the market movement parameters and thus it is difficult to draw conclusions on their effects on the MOE. However, the preliminary results of the plausibility models described in Chapter III are consistent with the literature in showing that market movements are a significant contributor to FMD spread.

B. CONTROL AREA AND SURVEILLANCE ZONE SIZES

The sizes of the control area and the surveillance zone were not as significant to our models as we expected at the beginning of our research. The size of the surveillance zone was always more significant than the size of the control area in our models. This is counterintuitive since movement restrictions are tighter and surveillance for the disease is conducted more frequently in the control areas than in the surveillance zones. It may be that since the disease parameters so dominated our models that the effects of these zone sizes seemed insignificant by comparison. Perhaps once we have a better understanding of the limits of the disease parameters, the sizes of these zones will have more impact on the models.

C. SURVEILLANCE

Of the 35 surveillance factors we model, two types of surveillance seem to have the greatest significance in our models. First, all forms of likeDairy surveillance consistently showed up as significant in our models. This is probably because surveillance is done so frequently on these types of premises that if the virus does infect one of them, it is detected quickly and therefore controls can be instituted quickly. Second, the delay until detection parameters—especially on likeDairy premises, but also generally and on traced premises—was significant to all of the regression models and most of the partition trees. This would indicate that one way to have an effect on limiting the size of the outbreak would be to prioritize dairy premises during lab testing so that the amount of time between initial testing and confirmation of the virus is kept to a minimum.

D. STARTING SCENARIOS

The most dangerous starting scenario in our model was the high animal density model, which is not surprising. Our model reinforces the choice made by other researchers, which is to focus on these areas of California when modeling this disease. However, all of the starting scenarios were able to generate large outbreaks given the correct combinations of the other parameters. Moreover, two scenarios—the high premises dense and the San Francisco Port—were able to consistently produce large outbreaks. This would suggest that the areas in Northern California could also be important to study in more detail. One could also argue that since the San Francisco Port is able to consistently produce large outbreaks, maintenance of surveillance resources at international ports is justified. Since we did not observe the same consistency of large outbreaks from the Los Angeles Port scenario, however, we feel that additional exploration of port scenarios is needed before making that claim.

E. DEPOPULATION RESOURCES

Two decision factors that were consistently significant to our models were the two depopulation resource parameters that described how many resources were available per day and how quickly those resources could be available. The partition trees split on these

parameters at about 12,000 animals per day and at a ramp-up time of less than nine days. These factors are probably so significant because there was not a preemptive culling strategy implemented in our model and because the local spread probabilities were not reduced based on detection of the disease on a premises. So, in order to control the disease, depopulation resources had to be readily available in large supply to quickly depopulate premises that became infected. If perfect biosecurity was established at the time of quarantine, and aerosol transmission was not a significant factor, then the disease should not spread from the premises. Therefore, our conclusions about the depopulation resources are also linked to the fact that we did not model the effect of biosecurity on the local spread parameters. Sensitivity analysis should be conducted to determine how these two parameters interact.

F. SUMMARY

Even though our models had relatively low adjusted R^2 values, we believe they still give us a fair amount of insight into the characteristics of the spread and control of an FMD outbreak in California. We believe that there are two major takeaways from our research for policymakers, and some for FMD researchers. We present the former below, and the latter in Chapter VII.

- The most important disease surveillance is done at likeDairy premises. We see the surveillance parameters of likeDairy premises as significant to both the detection time and size of outbreak regression models and partition trees. This is likely because these types of premises usually have personnel on staff who have daily contact with their animals and that the clinical signs of infection in cattle are generally easier to detect than in other species. These characteristics lead to decreased time until detection, which leads to quicker implementation of controls and smaller outbreaks. Continued research into how to make this type of surveillance as efficient as possible could have a significant impact on how large an outbreak becomes if it ever occurs in California.

- The size and availability of depopulation resources are significant in all of the size of outbreak models. Unlike many other authors' models and due to our understanding of the current views in California, we do not use preemptive depopulation in our model. Since we only depopulate detected premises and do not explore the effects of biosecurity on the local spread from those premises, we must accomplish depopulation as efficiently as possible to prevent or limit the spread of the disease. This requires the availability of large amounts of resources in a timely matter. Our model suggests the amount of resources necessary could be the ability to depopulate over 12,000 animals per day within nine days of the first detection of infected livestock premises. If the state does not plan on using preemptive depopulation, then this magnitude of depopulation resources should be readily available on a very short ramp-up timeline to facilitate the rapid control of an FMD outbreak.

VII. RECOMMENDATIONS FOR FUTURE RESEARCH

We feel that there are several areas where our research could be improved. When discussing the benefits of a simulation experimental design, Sanchez (2008, p. 83) writes,

> "This process typically follows an iterative cycle, where insights gained from simulation experiments can be used in many ways. Results can be used to evaluate or improve the simulation model. By identifying important factors, interactions, and nonlinear effects, the experimenter can improve their understanding, find robust solutions, or raise questions to be explored in subsequent experiments. Thresholds, plateaus, or other interesting features of the response surfaces might provide guidance about situations that are particularly good (or particularly bad)."

This thesis is one step in the iterative cycle of which Sanchez writes. During the rest of this chapter, we will discuss the changes that are needed or which would be interesting to explore in the ISP control file, the experimental design, the output statistics, and more general areas we feel should be further researched regarding the spread of FMD in California.

A. ISP CONTROL FILE

The development of the ISP control file was a difficult task due to the complexity and sheer number of parameters included in our simulation. Below is a list of the changes or fixes we recommend to those who would conduct follow-on research using ISP to model an outbreak of FMD in California.

- **Parameterize Dairy Tanker movement as "Fixed Routes":** Our results indicate that the diary premises in California have a significant impact on FMD control, and those premises also make up a large part of California's agricultural economic output. Our model could be improved by specifically modeling the movements of vehicles on and off of dairy premises. Data on tanker movements would be extremely useful, whether

gathered from industry groups, where the data resides, or from government organizations interested in controlling FMD.

- **Parameterize Airborne Spread:** Airborne spread can be an important factor for some FMD serotypes (Stevenson, 2012). Future models could benefit from adding predominant winds within the state. This may be especially important for areas of the state that are not within a "local spread" distance from a large farm, which can produce significant virus plumes, but may be downwind of one that is farther away.

- **Surveillance Zone Parameters:** In our base control file, we did not correctly use the option to preempt a premises being added to the surveillance zone if it had already been added to a control area. This did not affect our results since we corrected for this oversight in the output data. Future researchers should set the parameter "ExcludeFarmsInZones" to the zone name for the control area.

- **County Zones:** Radial zones are difficult to manage during an outbreak and would not generally be used under USDA guidelines (USDA, 2011). More likely, counties or similar-sized areas would be designated as certain zones or areas. ISP does not currently have the functionality to apply zones in this manner, but there may be ways to accomplish this in future updates to the software.

- **Restricting Movements on Farm Class:** Our model restricts all movements within a zone equally after the first detection of infected premises. This is perhaps not the best strategy given that some premises are more infectious, or have other applicable characteristics, than others. If strategies can be found that reduce the impact of movement restrictions on some premises, the overall impact on the California livestock industry could be reduced. The first step would be to quantify how much

movement restrictions actually hurt a livestock premises and then attempt to minimize the overall economic impact on the state, as opposed to surrogates such as the number of premises affected or infected.

- **Probabilities of Contact Between Farm Types:** Our model does not use the "RestrictOnAnimalType" or "RestrictOnFarmClass" parameters for direct and indirect movements. These parameters allow the user to specify restrictions to the destinations of specific movements. An example of this type of restriction is for direct contact movements originating from small swine premises to only be allowed to have destinations at other swine premises. Or, more specifically, for those same movements to only be allowed to have destinations at other small swine premises. We did not use them due to the complexity they add, as well as the fact that only one animal type is present on each of the premises in our data. However, adding these parameters would more closely resemble actual contact between premises.

- **Regional Movement Standstill:** Pineda-Krch et al. (2010) found that setting up a statewide movement ban on all livestock movements was beneficial in their research. While we believe that a statewide ban may not be necessary, given the large distances between livestock production regions within the state, we feel that future research should compare the impact of statewide "movement standstills" to more regionalized movement restrictions such as overlapping northern, central, and southern regions. ISP does have parameters to allow for such a comparison.

- **Regional California Dataset:** Due to the number of and geographic distances between the premises in our dataset, the development of smaller regional models, or a small mock "California," would allow closer examination of each factor. This may also help to more easily evaluate model behavior and identify problems with parameterization or bugs in the implementation of the software.

B. DESIGN OF THE EXPERIMENT (DOE)

The most difficult part of designing the experiment was in setting the high and low limits of each parameter studied. Based on the results of our model, we suggest the following modifications to the DOE:

- **Surveillance Rates:** The surveillance rates' high and low limits were generally set fairly wide apart in order to estimate their overall effect within the model. Now that we understand their importance to the model, more thought and expertise should be applied towards finding more realistic rates for each surveillance type. This could then give more fidelity to where limited surveillance resources should be applied.

- **Farm Probability of Transmission:** Our DOE currently applies low and high limits on farm probability of transmission from sheep and goats to 0% and 50%, respectively. We then apply a function to that probability in order to determine the probabilities for cattle and swine farms. After further review, this function for cattle may not allow probabilities to be as high as they should be when modeling direct and indirect contact between animals. We believe the exponent used should be closer to 15 instead of 1.82, in order to better model how much virus is shed by cattle by means other than aerosol, which is how we determine the current exponent used in the function.

- **Rate of Market Movement:** McLaws and Ribble (2007) propose that the factor that contributes most to an FMD outbreak becoming a large is virus movement through markets. However, we do not vary the number of farm-to-market movements per time period in our current design due to insufficient understanding of this parameter in the literature. Future research should vary this rate based on subject matter expert understanding or funding should be made available to collect data in order to better understand the spread of the virus prior to the first detection of infected premises.

- **Local Spread Multiplier Limits:** As discussed in Chapter VI, local spread is a dominant factor within our model. Since the first splits within all the partition trees we use in our analysis are on a local spread multiplier of approximately 1.6, which equates to a maximum distance band of roughly 4,800 m, it may merit checking the ISP software for idiosyncrasies at around the 5,000 m value. If such an anomaly exists within the software, our model may have more reliable results if the maximum local spread distance can be kept under that size.

- **Greater SME Input and Review:** The DOE high and low limits were set to widely vary the parameter settings as a first step in observing the effects of those factors. Now that we understand a bit more about these effects, SMEs should be used to narrow these ranges and therefore obtain more realistic outbreak results.

C. ADDITIONAL OUTPUT

In order to organize the simulation output for analysis, we use several scripts to read the output files developed by ISP during the simulation and calculate the MOEs we use for our analysis. Knowing the results of our analysis, we believe that three additional measures should be calculated by this script in order to further our understanding of the outbreaks simulated.

- **Day of last infection and/or day of last detection during each simulation iteration:** Currently, our model does not have a way to measure if or when the outbreak ended during the course of the simulation. For example, setting a time period of a certain number of days, say 28 days, since a detection would declare the epidemic over. Having this information would allow us to better understand the effectiveness of the control strategies.

- **The number of infected premises when the first detection occurs during each iteration:** We believe that we would better understand the relationship between the outbreak size and detection time if we knew how

fast the silent spread, the disease spread prior to first detection, is moving. Our belief is that when the outbreak spreads quickly, the virus is easier to detect. This is because we sample the susceptible population at a certain rate, and when more premises are infected, the time it takes to find an infected facility decreases. Having the number of infected premises and the types of those premises at the first detection would allow us to more fully explore this belief.

- **The locations of the randomly selected initially infected premises:** These locations should have been preserved in order to conduct some additional location-based analysis. We believe our starting scenarios do a good job of capturing the outbreak characteristics based on densities of animals or premises, but may not fully capture the geographic characteristics of California. Having more information about the exact initially infected premises location may better inform this area.

- **The projected number of infected premises when an iteration reaches the maximum number of infected premises:** Since our iterations were cut off when the number of infected premises reached 7,700, we had to develop a surrogate MOE to study the largest outbreaks. If the number of infected premises could be accurately projected, a surrogate MOE would not have to be used.

D. GENERAL RESEARCH

This thesis makes several assumptions because of either our lack of understanding or by an absence in the literature of several areas impacting a potential outbreak of FMD or any foreign animal disease in California. In this section, we describe two areas we feel need additional emphasis, research, or published information by the scientific community to inform the modeling of livestock diseases in the state.

- **Better knowledge of facility locations/species mix:** Because the data we used to construct our model were developed from publicly available, county-level aggregated statistics of livestock premises, they only

approximate the locations, sizes, animal types, and production types of the livestock premises in the state. Since ISP uses all of these characteristics to determine how the virus spreads, if the actual characteristics differ greatly from the approximate characteristics, the virus spread could also vary greatly.

E. KNOWLEDGE OF DIRECT AND INDIRECT MOVEMENT RATES AT LOCATIONS OUTSIDE OF CENTRAL CALIFORNIA:

Since the direct and indirect movement distances and probabilities were generated from a study of only central California, we may be over or underestimating the outbreaks in other areas of the state. Having better knowledge of these movements in other areas could help in better defining high-risk locations/regions of the state.

F. FINAL REMARKS

FMD is a fast-moving disease with potentially catastrophic consequences for California and the United States. It is important that policy makers are prepared to respond effectively and immediately if and when an outbreak occurs. Circumstances and details of an outbreak can greatly affect the behavior and consequences. There will not be time for model development during a crisis, so timely analysis requires having the appropriate models in reserve. This thesis takes an important step toward this ultimate objective.

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APPENDIX A. DESCRIPTION OF THE DESIGN OF EXPERIMENT

Factor name	Level Used in Plausiblity Model	Low Level	High Level	Factor Description	Methodology/Reference
MovementType1:NumberPerTimePeriod[114|214|314|24|34]	0.08	0.01	0.14	**Movement_Farm_Farm_Backyard:** Direct Contact movement rate from backyard premises (All Species). **Poisson** Distribution with means varied between low and high levels. Types affected: 114|214|314|24|34	Developed from Table 2 of Bates, et al (2001). High and low levels equal the high and low 95% CI from the table divided by 30 to get a daily rate. Premise type in table is Backyard.
MovementType2:NumberPerTimePeriod[310]	0.29	0.01	0.56	**Movement_Farm_Farm_Goat:** Direct Contact movement rate from Goat premises. **Poisson** Distribution with means varied between low and high levels. Types affected: 310	Developed from Table 2 of Bates, et al (2001). High and low levels equal the high and low 95% CI from the table divided by 30 to get a daily rate. Premise type in table is Goat.
MovementType3:NumberPerTimePeriod[211|213]	0.32	0.01	0.6267	**Movement_Farm_Farm_Sheep:** Direct Contact movement rate from Sheep premises. **Poisson** Distribution with means varied between low and high	Developed from Table 2 of Bates, et al (2001). High and low levels equal the high and low 95% CI from the table divided by 30 to get a daily rate. Premise type in table is
MovementType4:NumberPerTimePeriod[51|61]	0.03	0.0167	0.0433	**Movement_Farm_Farm_BeefS:** Direct Contact movement rate from smal Beef premises. **Poisson** Distribution with means varied between low and high levels. Types affected: 51|61	Developed from Table 2 of Bates, et al (2001). High and low levels equal the high and low 95% CI from the table divided by 30 to get a daily rate. Premise type in table is Beef < 250.
MovementType5:NumberPerTimePeriod[53|63]	0.06	0.01	0.1	**Movement_Farm_Farm_BeefL:** Direct Contact movement rate from large Beef premises. **Poisson** Distribution with means varied between low and high levels. Types affected: 53|63	Developed from Table 2 of Bates, et al (2001). High and low levels equal the high and low 95% CI from the table divided by 30 to get a daily rate. Premise type in table is Beef >= 250.
MovementType6:NumberPerTimePeriod[31|32]	0.27	0.1433	0.4033	**Movement_Farm_Farm_DairyS:** Direct Contact movement rate from Small Dairy premises. **Poisson** Distribution with means varied between low and high levels. Types affected: 31|32	Developed from Table 2 of Bates, et al (2001). High and low levels equal the high and low 95% CI from the table divided by 30 to get a daily rate. Premise type in table is Dairy < 1000.
MovementType7:NumberPerTimePeriod[33]	0.55	0.3967	0.6967	**Movement_Farm_Farm_DairyL:** Direct Contact movement rate from Large Dairy premises. **Poisson** Distribution with means varied between low and high levels. Types affected: 33	Developed from Table 2 of Bates, et al (2001). High and low levels equal the high and low 95% CI from the table divided by 30 to get a daily rate. Premise type in table is Dairy >= 2000.
MovementType8:NumberPerTimePeriod[41]	0.02	0.01	0.0367	**Movement_Farm_Farm_Calf_HeiferS:** Direct Contact movement rate from Small Calf/Heifer premises. **Poisson** Distribution with means varied between low and high levels. Types affected: 41	Developed from Table 2 of Bates, et al (2001). High and low levels equal the high and low 95% CI from the table divided by 30 to get a daily rate. Premise type in table is Calf/Heifer < 250.
MovementType9:NumberPerTimePeriod[43|73]	0.99	0.01	1.96	**Movement_Farm_Farm_Calf_HeiferL:** Direct Contact movement rate from Large Calf/Heifer premises. **Poisson** Distribution with means varied between low and high levels. Types affected: 43|73	Developed from Table 2 of Bates, et al (2001). High and low levels equal the high and low 95% CI from the table divided by 30 to get a daily rate. Premise type in table is Calf/Heifer >= 250.
MovementType10:NumberPerTimePeriod[121|131|151|161]	0.16	0.0367	0.2833	**Movement_Farm_Farm_SwineS:** Direct Contact movement rate from Small Swine premises. **Poisson** Distribution with means varied between low and high levels. Types affected: 121|131|151|161	Developed from Table 2 of Bates, et al (2001). High and low levels equal the high and low 95% CI from the table divided by 30 to get a daily rate. Premise type in table is Swine < 2000.
MovementType11:NumberPerTimePeriod[153|163]	0.67	0.0067	1.3267	**Movement_Farm_Farm_SwineL:** Direct Contact movement rate from Large Swind premises. **Poisson** Distribution with means varied between low and high levels. Types affected: 153|163	Developed from Table 2 of Bates, et al (2001). High and low levels equal the high and low 95% CI from the table divided by 30 to get a daily rate. Premise type in table is Swine >= 2000.
MovementType14:NumberPerTimePeriod[41]	0.03	0.01	0.046	**IDMovement_Size1:** Indirect Contact movement rate for Small Calf/Heifer premises. Poisson Distribution with means varied between low and high levels. Types affected: 41	Developed from Table 3 of Bates, et al (2001). Employee and Friend Visitor types were removed due to our feeling that the probabilities of spread from those two types are different from the rest of the types, and that they are accounted for in the "Local Spread" of the disease. High and low levels equal the high and low 95% CI from the table divided by 30 to get a daily rate. If the low 95% Confidence bound was less than 0 after removing Employees and Friends, .01 was used instead.
MovementType15:NumberPerTimePeriod[24|34|114|214|314|310|211|213|51|61|53|63|121|131|151|161]	0.16	0.01	0.3143	**IDMovement_Size2:** Indirect Contact movement rate for a group of premise types that have the same order of magnitude mean rate. Poisson Distribution with means varied between low and high levels. Types affected: 24|34|114|214|314|310|211|213|51|61|53|63|121|131|151|161	Developed from Table 3 of Bates, et al (2001). Employee and Friend Visitor types were removed due to our feeling that the probabilities of spread from those two types are different from the rest of the types, and that they are accounted for in the "Local Spread" of the disease. High and low levels equal the maximum high and and minimum low 95% CI of all of the from the table divided by 30 to get a daily rate. If the low 95% Confidence bound was less than 0 after removing Employees and Friends, .01 was used instead.
MovementType16:NumberPerTimePeriod[153|163]	0.82	0.01	1.626	**IDMovement_Size3:** Indirect Contact movement rate for a group of premise types that have the same order of magnitude mean rate. Poisson Distribution with means varied between low and high levels. Types affected: 153|163	Developed from Table 3 of Bates, et al (2001). Employee and Friend Visitor types were removed due to our feeling that the probabilities of spread from those two types are different from the rest of the types, and that they are accounted for in the "Local Spread" of the disease. High and low levels equal the maximum high and and minimum low 95% CI of all of the from the table divided by 30 to get a daily rate. If the low 95% Confidence bound was less than 0 after removing Employees and Friends, .01 was used instead.
MovementType17:NumberPerTimePeriod[31|32|43|73]	1.02	0.01	2.0343	**IDMovement_Size4:** Indirect Contact movement rate for a group of premise types that have the same order of magnitude mean rate. Poisson Distribution with means varied between low and high levels. Types affected: 31|32|43|73	Developed from Table 3 of Bates, et al (2001). Employee and Friend Visitor types were removed due to our feeling that the probabilities of spread from those two types are different from the rest of the types, and that they are accounted for in the "Local Spread" of the disease. High and low levels equal the maximum high and and minimum low 95% CI of all of the from the table divided by 30 to get a daily rate. If the low 95% Confidence bound was less than 0 after removing Employees and Friends, .01 was used instead.
MovementType18:NumberPerTimePeriod[33]	0.95	0.862	1.0413	**IDMovement_Size5:** Indirect Contact movement rate for Large Dairy premises. Poisson Distribution with means varied between low and high levels. Types affected: 33	Developed from Table 3 of Bates, et al (2001). Employee and Friend Visitor types were removed due to our feeling that the probabilities of spread from those two types are different from the rest of the types, and that they are accounted for in the "Local Spread" of the disease. High and low levels equal the high and low 95% CI from the table divided by 30 to get a daily rate. If the low 95% Confidence bound was less than 0 after removing Employees and Friends, .01 was used instead.

AllMovements:MovementDistance	**1.13**	**0.25**	**2**	A multiplier applied to the distance bands for all movement types simultaneously.	Developed from Table 3 of Bates, et al (2001). Probabilities of the virus moving to these distances remains fixed across all movement types, but refer to the updated movement bands after the multiplier has been applied. A multiplier = 1 will produce movement bands (in meters) of: 0-19000, 19001-39000, 39001-59000, 59001-79000, 79001-99000, 99001-119000, 119001-139000, 139001-159000, 159001-179000.
AllFarms:ProbabilityOfTransmission	**0.30**	**0.1**	**0.5**	The constant to be used as the basis to calculate the probability of transmission for all farm to farm movements (Direct and Indirect). This number is an input to functions to calculate the probability of transmission for different species.	High and low levels based on subject matter expert opinion for farm to farm direct or indirect contact for sheep/goats. This constant is then an input (p) into the following functions based on species type on the source farm. > Cattle POT = 1-(1-p)^1.82 > Swine POT = 1-(1-p)^80
AllMarkets:ProbabilityOfTransmission	**0.75**	**0.5**	**1**	The constant to be used as the basis to calculate the probability of transmission for all farm to market and market to farm movements.	High and low levels based on subject matter expert opinion for farm to market and market to farm direct contact.
LocalSpread1:Multiplier	**1.13**	**0.25**	**2**	A multiplier applied to the distance bands for local spread.	Reference: Personal communication with Mark Stevenson on 11 Apr 2012. Probabilities of the virus moving to these distances remains fixed, but refer to the updated movement bands after the multiplier has been applied. A multiplier = 1 will produce movement bands (in meters) of: 0-1000, 1001-2000, 2001-3000. Note: The probabilities of transmission for Local Spread change over time. Local spread initiates when the farm starts showing clinical signs and stops after 6 days.
LocalSpread1:RelativeSusceptibility[swine]	**0.01**	**0.001**	**0.1**	Suceptability of swine to local spread relative to cattle.	Reference (Donaldson et al., 2001; Alexanderson and Donaldson, 2002).
LocalSpread1:RelativeSusceptibility[sheep]	**0.05**	**0.005**	**0.5**	Suceptability of sheep to local spread relative to cattle.	Reference (Donaldson et al., 2001; Alexanderson and Donaldson, 2002).
LocalSpread1:RelativeSusceptibility[goat]	**0.05**	**0.005**	**0.5**	Suceptability of goat to local spread relative to cattle.	Reference (Donaldson et al., 2001; Alexanderson and Donaldson, 2002).
Infectivity1:TimeToClinicalSigns	**4.38**	**1**	**8**	The Beta value of a LogLogistic Curve with parameters (2, Beta, 4.1436) describing the time until clinical signs are evident on the premise.	Reference Sanson, et al (2006b). Table 2 shows a cumulative probability table, which we fit to a LogLogistic Curve with parameters (0,beta=4.3770,alpha=4.1436) The high and low levels adjust the B value are based on subject matter expert opinion.
Infectivity1:Infectivity[][][]:DecreaseStart	**17.00**	**12**	**22**	The day after infection when infectivity begins to decrease on the premise.	Reference Sanson, et al (2006b). Delphi Conference estimated that premise would be most infectious on day 16 after initial infection, and the infectiousness would decrease linearly until day 33. Here we vary the start and end of the infectiousness decline by +/- 5 days.
Infectivity1:Infectivity[][][]:DecreaseEnd	**33.00**	**28**	**38**	The day when the premise becomes immune.	
Zone2:OutsideRadius1:ControlArea	**10001**	**1**	**20000**	**Control Measure:** Outside radius of the control area in meters.	Reference APHIS (2012), Ready Reference Guide—Quarantine, Movement Control, and Continuity of Business. Developed radii by adding or subtracting a reasonable distance from published minimum guidelines for small control areas. Once other parameter limits have been better evaluated, larger zones should be studied within the design.
Zone3:OutsideRadius1:VaccZone	**10000**	**0**	**20000**	**Control Measure:** Outside radius of the vaccination zone in meters.	
Zone4:OutsideRadius1:SurvZone	**25000**	**0**	**50000**	**Control Measure:** Outside radius of the Surveillance zone in meters.	
Resource1:PerTimePeriod	**1.00**	**0.5**	**2**	**DepopResource:** a multiplier applied to the number of animals able to be culled in a day. When multiplier = 1, the animals culled per day (regardless of species) = 20,000 animals after full utilization day, and 2000 animals until then.	20000 animals developed from the total number of animals culled during the U.K. FMD outbreak (4.5M) and dividing by the number of months the outbreak lasted multiplied by 30 to give a daily rate. i.e.: 20000 = 4.5M/(7.5*30).
Resource1:TimePeriodStart2:FullUtilization	**11.00**	**2**	**21**	**DepopResource:** Day that all Resources are available. Up until this day, resources are available at 10% of full capacity.	Tests the importance of a quick ramp up to full capacity. Early testing with full utilization longer than 21 days led to significant increases in the runtime of the design of experiment.
Resource2:PerTimePeriod	**1.00**	**0.5**	**2**	**VaccinationResource:** a multiplier applied to the number of animals able to be vaccinated in a day. When multiplier = 1, the animals vaccinated per day (regardless of species) = 20,000 animals after full utilization day, and	Same as depopulation. Estimated that the capacity to vaccinate would be roughly equivalent to depopulation.
Resource2:TimePeriodStart2:FullUtilization	**11.00**	**2**	**21**	**VaccinationResource:** Day that all Resources are available. Up until this day, resources are available at 10% of full capacity.	Tests the importance of a quick ramp up to full capacity. Same high and low levels as depopulation resource.
Surveillance1:VisitDelay:GenSurv	**6.00**	**2**	**10**	**GeneralSurveillance:** A probability distribution describing the number of time periods that will pass before a farm is visited prior to being placed on the surveillance list following a detected farm in the area. Poisson Distribution with means varied between low and high levels.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance1:VisitFrequency:GenSurv	**6.50**	**3**	**10**	**GeneralSurveillance:** A probability distribution describing the number of time periods that will pass between visits to a farm following the first visit (described by the VisitDelay) prior to a farm being placed on the surveillance list. Poisson Distribution with means varied between low and high levels.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.

Surveillance1:DelayToDetection:GenSurv	**4.50**	**2**	**7**	**GeneralSurveillance:** A probability distribution returning the number of time periods from when the visit occurred to when that farm will receive the detected state (prior to a farm being placed on the surveillance list). Poisson Distribution with means varied between low and high levels.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance1:DetectionProbability[][][]:GenSurv	**0.50**	**0**	**0.99**	**GeneralSurveillance:** A function describing the probability of an infected farm being detected at each visit by the number of time periods since the farm was infected. In our case, the function is constant, but would vary between the Lo and Hi values shown.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance1:DetectionProbability[][][sheep]:GenSurv	**0.48**	**0**	**0.95**	**GeneralSurveillance:** A function describing the probability of an infected **Sheep** farm being detected at each visit by the number of time periods since the farm was infected. In our case, the function is constant, but would vary between the Lo and Hi values shown.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance2:VisitDelay:GeneralAfterFirstDetection	**4.50**	**2**	**7**	**GeneralSurveillance_AfterDetect:** A probability distribution describing the number of time periods that will pass before a farm is visited after being placed on the surveillance list following a detected farm in the area. Poisson Distribution with means varied between low and high levels.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance2:VisitFrequency:GeneralAfterFirstDetection	**4.50**	**2**	**7**	**GeneralSurveillance_AfterDetect:** A probability distribution describing the number of time periods that will pass between visits to a farm following the first visit (described by the VisitDelay) while a farm is on the surveillance list. Poisson Distribution with means varied between low and high levels.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance2:DelayToDetection:GeneralAfterFirstDetection	**3.00**	**1**	**5**	**GeneralSurveillance_AfterDetect:** A probability distribution returning the number of time periods from when the visit occurred to when that farm will receive the detected state. Poisson Distribution with means varied between low and high levels.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance2:DetectionProbability[][][]:GeneralAfterFirstDetection	**0.90**	**0.8**	**0.99**	**GeneralSurveillance_AfterDetect:** A function describing the probability of an infected farm being detected at each visit by the number of time periods since the farm was infected. In our case, the function is constant, but would vary between the Lo and Hi values shown.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance2:DetectionProbability[][][sheep]:GeneralAfterFirstDetection	**0.83**	**0.7**	**0.95**	**GeneralSurveillance_AfterDetect:** A function describing the probability of an infected **Sheep** farm being detected at each visit by the number of time periods since the farm was infected. In our case, the function is constant, but would vary between the Lo and Hi values shown.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance3:VisitDelay:GeneralSurv_Dairy_before	**1.75**	**0.5**	**3**	**GeneralSurv_Dairy_before:** A probability distribution describing the number of time periods that will pass before a farm is visited after being placed on the surveillance list following a detected farm in the area. Poisson Distribution with means varied between low and high levels.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance3:VisitFrequency:GeneralSurv_Dairy_before	**1.75**	**0.5**	**3**	**GeneralSurv_Dairy_before:** A probability distribution describing the number of time periods that will pass between visits to a farm following the first visit (described by the VisitDelay) while a farm is on the surveillance list. Poisson Distribution with means varied between low and high levels.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance3:DelayToDetection:GeneralSurv_Dairy_before	**3.00**	**1**	**5**	**GeneralSurv_Dairy_before:** A probability distribution returning the number of time periods from when the visit occurred to when that farm will receive the detected state. Poisson Distribution with means varied between low and high levels.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance3:DetectionProbability[][][]:GeneralSurv_Dairy_before	**0.75**	**0.5**	**0.99**	**GeneralSurv_Dairy_before:** A function describing the probability of an infected farm being detected at each visit by the number of time periods since the farm was infected. In our case, the function is constant, but would vary between the Lo and Hi values shown.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance4:VisitDelay:GeneralSurv_Dairy_after	**1.25**	**0.5**	**2**	**GeneralSurv_Dairy_after:** A probability distribution describing the number of time periods that will pass before a farm is visited after being placed on the surveillance list following a detected farm in the area. Poisson Distribution with means varied between low and	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance4:VisitFrequency:GeneralSurv_Dairy_after	**1.25**	**0.5**	**2**	**GeneralSurv_Dairy_after:** A probability distribution describing the number of time periods that will pass between visits to a farm following the first visit (described by the VisitDelay) while a farm is on the	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance4:DelayToDetection:GeneralSurv_Dairy_after	**1.75**	**0.5**	**3**	**GeneralSurv_Dairy_after:** A probability distribution returning the number of time periods from when the visit occurred to when that farm will receive the detected state. Poisson Distribution with means varied between low and high levels.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance4:DetectionProbability[][][]:GeneralSurv_Dairy_after	**0.90**	**0.8**	**0.99**	**GeneralSurv_Dairy_after:** A function describing the probability of an infected farm being detected at each visit by the number of time periods since the farm was infected. In our case, the function is constant, but would vary between the Lo and Hi values shown.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.

Surveillance5:VisitDelay:ControlArea	**2.75**	**0.5**	**5**	**Surv_ControlArea:** A probability distribution describing the number of time periods that will pass before a farm is visited after being placed on the surveillance list following a detected farm in the area. Poisson Distribution with means varied between low and high levels.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance5:VisitFrequency:ControlArea	**4.00**	**1**	**7**	**Surv_ControlArea:** A probability distribution describing the number of time periods that will pass between visits to a farm following the first visit (described by the VisitDelay) while a farm is on the surveillance list. Poisson Distribution with means varied between low and high levels.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance5:DelayToDetection:ControlArea	**1.25**	**0.5**	**2**	**Surv_ControlArea:** A probability distribution returning the number of time periods from when the visit occurred to when that farm will receive the detected state. Poisson Distribution with means varied between low and high levels.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance5:DetectionProbability[][][]:ControlArea	**0.90**	**0.8**	**0.99**	**Surv_ControlArea:** A function describing the probability of an infected farm being detected at each visit by the number of time periods since the farm was infected. In our case, the function is constant, but would vary between the Lo and Hi values shown.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance5:DetectionProbability[][][sheep]:ControlArea	**0.83**	**0.7**	**0.95**	**Surv_ControlArea:** A function describing the probability of an infected **Sheep** farm being detected at each visit by the number of time periods since the farm was infected. In our case, the function is constant, but would vary between the Lo and Hi values shown.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance6:VisitDelay:SurvZone	**3.50**	**2**	**5**	**Surv_Zone:** A probability distribution describing the number of time periods that will pass before a farm is visited after being placed on the surveillance list following a detected farm in the area. Poisson Distribution with means varied between low and high levels.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance6:VisitFrequency:SurvZone	**4.50**	**2**	**7**	**Surv_Zone:** A probability distribution describing the number of time periods that will pass between visits to a farm following the first visit (described by the VisitDelay) while a farm is on the surveillance list. Poisson Distribution with means varied between low and high levels.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance6:DelayToDetection:SurvZone	**1.50**	**1**	**2**	**Surv_Zone:** A probability distribution returning the number of time periods from when the visit occurred to when that farm will receive the detected state. Poisson Distribution with means varied between low and high levels.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance6:DetectionProbability[][][]:SurvZone	**0.90**	**0.8**	**0.99**	**Surv_Zone:** A function describing the probability of an infected farm being detected at each visit by the number of time periods since the farm was infected. In our case, the function is constant, but would vary between the Lo and Hi values shown.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance6:DetectionProbability[][][sheep]:SurvZone	**0.83**	**0.7**	**0.95**	**Surv_Zone:** A function describing the probability of an infected **Sheep** farm being detected at each visit by the number of time periods since the farm was infected. In our case, the function is constant, but would vary between the Lo and Hi values shown.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance7:VisitDelay:Trace	**4.00**	**1**	**7**	**Surv_Trace:** A probability distribution describing the number of time periods that will pass before a farm is visited after being placed on the surveillance list following a detected farm in the area. Poisson Distribution with means varied between low and high levels.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance7:VisitFrequency:Trace	**4.00**	**1**	**7**	**Surv_Trace:** A probability distribution describing the number of time periods that will pass between visits to a farm following the first visit (described by the VisitDelay) while a farm is on the surveillance list. Poisson Distribution with means varied between low and high levels.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance7:DelayToDetection:Trace	**3.00**	**1**	**5**	**Surv_Trace:** A probability distribution returning the number of time periods from when the visit occurred to when that farm will receive the detected state. Poisson Distribution with means varied between low and high levels.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance7:DetectionProbability[][][]:Trace	**0.90**	**0.8**	**0.99**	**Surv_Trace:** A function describing the probability of an infected farm being detected at each visit by the number of time periods since the farm was infected. In our case, the function is constant, but would vary between the Lo and Hi values shown.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Surveillance7:DetectionProbability[][][sheep]:Trace	**0.83**	**0.7**	**0.95**	**Surv_Trace:** A function describing the probability of an infected **Sheep** farm being detected at each visit by the number of time periods since the farm was infected. In our case, the function is constant, but would vary between the Lo and Hi values shown.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012.
Tracing1:ProbMovementForgotten[][]	**0.43**	**0.05**	**0.8**	**Tracing:** a probability that the infectious movement will be **forgotten** by the farmer and therefore never traced. Here, this is the same for all movement types.	Used a wide range to test importance of this factor
Tracing1:TracingDelay[][]	**3.75**	**0.5**	**7**	**Tracing:** The mean of a Poisson distribution of the number of time periods it takes to trace the infectious movement. Here, this is the same for all movement types.	Used a wide range to test importance of this factor
MovementRestriction1:ProbMovementRestricted:ControlArea	**0.92**	**0.85**	**0.99**	**MovementControlControlArea:** The probability that the movement defined in this movement restriction, will be prevented.	Bates, et al (2003) showed predicted movement restriction disregard from 5-12% of movements in the control area.

MovementRestriction2:ProbMovementRestricted:SurvZone	**0.85**	**0.7**	**0.99**	**MovementControl_Surv:** The probability that the movement defined in this movement restriction, will be prevented.	Bates, et al (2003). We estimated that restrictions outside of the control area may be disregarded at a higher percentage than within the control area.
Binary Variables					
Vaccination1:FarmClasses:DairyOnly		**0**	**1**	**Vacc_Zone:** Binary. If 0, then all cattle will be vaccinated. If 1, only Dairy premises, Dairy calf ranches, and feedlots will be vaccinated.	Based on SME opinion. Adapted from general guidelines provided by Pam Hullinger during personal conversation on 12 Apr 2012. If there is a 1 here, this then applies to farm types ("31 | 32 | 33 | 51 | 53 | 73").
MovementRestriction3:ProbMovementRestricted:StopMarkets		**0**	**0.995**	**StopMarkets: Binary variable defining the movement restrictions put on the market will be set for all markets (hi value) or only markets in a control area or surveillance zone.**	Tests whether shutting down all markets or only those in the control area is a better strategy.

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APPENDIX B. INTERSPREADPLUS CONTROL FILE

```
;InteSpread Plus Control File Editor v2
;Created: 4/23/2012 4:39:57 PM

[Model]
IterationCount=100
TimePeriodCount=100
Seed=1234
RandomGeneratorName=C
MaxInfectedFarms=7700
UserDefinedStateCount=14
FarmFileCount=1
ContactLocationsCount=1
SetStateCount=1
MovementTypeCount=18
RouteCount=0
FixedRouteCount=0
LocalSpreadCount=1
AirborneSpreadCount=0
RecrudescenceCount=0
InfectivityCount=1
ZoneCount=5
ResourceCount=3
DepopulationCount=1
VaccinationCount=1
SurveillanceCount=7
TracingCount=1
MovementRestrictionCount=3
MovementStandstillCount=0
RestockingCount=0
OutputCount=6
UserDefinedState1=in_control_area
UserDefinedState2=processing_depop
UserDefinedState3=depopulated
UserDefinedState4=delayed_depop
UserDefinedState5=in_vacc_zone
UserDefinedState6=processing_vacc
UserDefinedState7=vaccinated
UserDefinedState8=delayed_vacc
UserDefinedState9=in_surv_zone
UserDefinedState10=waiting_depop
UserDefinedState11=waiting_vacc
UserDefinedState12=likeDairy_beforeDetect
```

UserDefinedState13=likeDairy_afterDetect
UserDefinedState14=likeDairy

[FarmFile1]
Pathname=.\CalFarmFinal_withDensity.txt
NumberOfColumns=17
Column1=farmid
Column2=farm_class
Column3=user_defined FIPS_Code long
Column4=user_defined UTM_Zone double
Column5=animals cattle
Column6=animals swine
Column7=animals sheep
Column8=animals goat
Column9=animals other
Column10=user_defined Type_Name string
Column11=user_defined premise_3k long
Column12=user_defined premise_10k long
Column13=user_defined premise_20k long
Column14=user_defined animal_3k long
Column15=user_defined animal_10k long
Column16=user_defined animal_20k long
Column17=coordinates

[ContactLocations1]
ContactLocationsName=Markets_Combined
Pathname=.\CAMarket_combined.txt

[EpidemicHistory]
StateFileName=.\STATE_Port_LA11.txt
HistoryEndTimePeriod=1
InfectedFarmHandling=include_always

[SetState1]
TimePeriod=1
Coordinates=.\ZoneCalUTM.txt
FarmClasses=31 | 32 | 33 | 51 | 53 | 73
ProportionOfFarms=1.0
StatesToSet=likeDairy

[MovementType1]
MovementName=Movement_Farm_Farm_Backyard
TimePeriodStart=1
TimePeriodStop=1000
NumberPerTimePeriod=Constant 0

NumberOfDirectContacts=Constant 1
DestinationType=farm
MovementDistance=1,0,0.615,0.11,0.025,0.06,0.01,0.035,0.01,0,0.135;0,0,19000,39000,
59000,79000,99000,119000,139000,159000,179000
ProbabilityOfTransmission=Constant 0.2
NumberPerTimePeriod[114|214|314|24|34]=Poisson 0.049

[MovementType2]
MovementName=Movement_Farm_Farm_Goat
TimePeriodStart=1
TimePeriodStop=1000
NumberPerTimePeriod=Constant 0
NumberOfDirectContacts=Constant 1
DestinationType=farm
MovementDistance=1,0,0.365,0.16,0.09,0.035,0.01,0,0.015,0.025,0.3;0,0,19000,39000,5
9000,79000,99000,119000,139000,159000,179000
ProbabilityOfTransmission=Constant 0.2
NumberPerTimePeriod[310]=Poisson 0.115

[MovementType3]
MovementName=Movement_Farm_Farm_Sheep
TimePeriodStart=1
TimePeriodStop=1000
NumberPerTimePeriod=Constant 0
NumberOfDirectContacts=Constant 1
DestinationType=farm
MovementDistance=1,0,0.365,0.16,0.09,0.035,0.01,0,0.015,0.025,0.3;0,0,19000,39000,5
9000,79000,99000,119000,139000,159000,179000
ProbabilityOfTransmission=Constant 0.2
NumberPerTimePeriod[211|213]=Poisson 0.154

[MovementType4]
MovementName=Movement_Farm_Farm_BeefS
TimePeriodStart=1
TimePeriodStop=1000
NumberPerTimePeriod=Constant 0
NumberOfDirectContacts=Constant 1
DestinationType=farm
MovementDistance=1,0,0.39,0.22,0.125,0.055,0.025,0.01,0.02,0.015,0.14;0,0,19000,390
00,59000,79000,99000,119000,139000,159000,179000
ProbabilityOfTransmission=Constant 0.338
NumberPerTimePeriod[51|61]=Poisson 0.02

[MovementType5]
MovementName=Movement_Farm_Farm_BeefL

TimePeriodStart=1
TimePeriodStop=1000
NumberPerTimePeriod=Constant 0
NumberOfDirectContacts=Constant 1
DestinationType=farm
MovementDistance=1,0,0.39,0.22,0.125,0.055,0.025,0.01,0.02,0.015,0.14;0,0,19000,390
00,59000,79000,99000,119000,139000,159000,179000
ProbabilityOfTransmission=Constant 0.338
NumberPerTimePeriod[53|63]=Poisson 0.038

[MovementType6]
MovementName=Movement_Farm_Farm_DairyS
TimePeriodStart=1
TimePeriodStop=1000
NumberPerTimePeriod=Constant 0
NumberOfDirectContacts=Constant 1
DestinationType=farm
MovementDistance=1,0,0.57,0.255,0.035,0.01,0.005,0.01,0.005,0.005,0.105;0,0,19000,3
9000,59000,79000,99000,119000,139000,159000,179000
ProbabilityOfTransmission=Constant 0.338
NumberPerTimePeriod[31|32]=Poisson 0.164

[MovementType7]
MovementName=Movement_Farm_Farm_DairyL
TimePeriodStart=1
TimePeriodStop=1000
NumberPerTimePeriod=Constant 0
NumberOfDirectContacts=Constant 1
DestinationType=farm
MovementDistance=1,0,0.57,0.255,0.035,0.01,0.005,0.01,0.005,0.005,0.105;0,0,19000,3
9000,59000,79000,99000,119000,139000,159000,179000
ProbabilityOfTransmission=Constant 0.338
NumberPerTimePeriod[33]=Poisson 0.298

[MovementType8]
MovementName=Movement_Farm_Farm_Calf_HeiferS
TimePeriodStart=1
TimePeriodStop=1000
NumberPerTimePeriod=Constant 0
NumberOfDirectContacts=Constant 1
DestinationType=farm
MovementDistance=1,0,0.41,0.145,0.205,0,0,0,0.02,0,0.22;0,0,19000,39000,59000,7900
0,99000,119000,139000,159000,179000
ProbabilityOfTransmission=Constant 0.338
NumberPerTimePeriod[41]=Poisson 0.017

[MovementType9]
MovementName=Movement_Farm_Farm_Calf_HeiferL
TimePeriodStart=1
TimePeriodStop=1000
NumberPerTimePeriod=Constant 0
NumberOfDirectContacts=Constant 1
DestinationType=farm
MovementDistance=1,0,0.41,0.145,0.205,0,0,0,0.02,0,0.22;0,0,19000,39000,59000,7900
0,99000,119000,139000,159000,179000
ProbabilityOfTransmission=Constant 0.338
NumberPerTimePeriod[43|73]=Poisson 0.657

[MovementType10]
MovementName=Movement_Farm_Farm_SwineS
TimePeriodStart=1
TimePeriodStop=1000
NumberPerTimePeriod=Constant 0
NumberOfDirectContacts=Constant 1
DestinationType=farm
MovementDistance=1,0,0.315,0.29,0.02,0.05,0.12,0.045,0.015,0,0.145;0,0,19000,39000,
59000,79000,99000,119000,139000,159000,179000
ProbabilityOfTransmission=Constant 0.9999
NumberPerTimePeriod[121|131|151|161]=Poisson 0.088

[MovementType11]
MovementName=Movement_Farm_Farm_SwineL
TimePeriodStart=1
TimePeriodStop=1000
NumberPerTimePeriod=Constant 0
NumberOfDirectContacts=Constant 1
DestinationType=farm
MovementDistance=1,0,0.315,0.29,0.02,0.05,0.12,0.045,0.015,0,0.145;0,0,19000,39000,
59000,79000,99000,119000,139000,159000,179000
ProbabilityOfTransmission=Constant 0.9999
NumberPerTimePeriod[153|163]=Poisson 0.334

[MovementType12]
MovementName=Movement_market-farm
TimePeriodStart=1
TimePeriodStop=1000
NumberPerTimePeriod=Constant 0
NumberOfDirectContacts=Constant 0
DestinationType=farm
RestrictOnAnimals=N

MovementDistance=1,0,0.383,0.202,0.119,0.061,0.013,0.069,0.04,0.021,0.092;0,0,19000
,39000,59000,79000,99000,119000,139000,159000,179000
ProbabilityOfTransmission=Constant 0.8
MaxResampleAttempts=0

[MovementType13]
MovementName=Movement_farm-market
TimePeriodStart=1
TimePeriodStop=1000
NumberPerTimePeriod=Poisson 0.1
NumberOfDirectContacts=Constant 1
DestinationType=contact_location
ContactLocationControlName=Markets_Combined
RestrictOnAnimals=N
MovementDistance=1,0,0.546,0.216,0.167,0.018,0.005,0.014,0.004,0.006,0.024;0,0,1900
0,39000,59000,79000,99000,119000,139000,159000,179000
ProbabilityOfTransmission=Constant 0.8
MaxResampleAttempts=0
SourceOfSecondaryContacts=source
NumberOfSecondaryContacts[Movement_market-farm]=Poisson 1

[MovementType14]
MovementName=IDMovement_Size1
TimePeriodStart=1
TimePeriodStop=1000
NumberPerTimePeriod=Constant 0
NumberOfDirectContacts=Constant 1
DestinationType=farm
MovementDistance=1,0,0.44,0.3283,0.1367,0.055,0.011,0.029;0,0,9000,19000,29000,39
000,49000,59000
ProbabilityOfTransmission=Constant 0.338
NumberPerTimePeriod[41]=Poisson 0.005

[MovementType15]
MovementName=IDMovement_Size2
TimePeriodStart=1
TimePeriodStop=1000
NumberPerTimePeriod=Constant 0
NumberOfDirectContacts=Constant 1
DestinationType=farm
MovementDistance=1,0,0.44,0.3283,0.1367,0.055,0.011,0.029;0,0,9000,19000,29000,39
000,49000,59000
ProbabilityOfTransmission=Constant 0.338
NumberPerTimePeriod[24|34|114|214|314|310|211|213|51|61|53|63|121|131|151|161]=Poi
sson 0.0252

[MovementType16]
MovementName=IDMovement_Size3
TimePeriodStart=1
TimePeriodStop=1000
NumberPerTimePeriod=Constant 0
NumberOfDirectContacts=Constant 1
DestinationType=farm
MovementDistance=1,0,0.44,0.3283,0.1367,0.055,0.011,0.029;0,0,9000,19000,29000,39000,49000,59000
ProbabilityOfTransmission=Constant 0.338
NumberPerTimePeriod[153|163]=Poisson 0.1853

[MovementType17]
MovementName=IDMovement_Size4
TimePeriodStart=1
TimePeriodStop=1000
NumberPerTimePeriod=Constant 0
NumberOfDirectContacts=Constant 1
DestinationType=farm
MovementDistance=1,0,0.44,0.3283,0.1367,0.055,0.011,0.029;0,0,9000,19000,29000,39000,49000,59000
ProbabilityOfTransmission=Constant 0.338
NumberPerTimePeriod[31|32|43|73]=Poisson .4294

[MovementType18]
MovementName=IDMovement_Size5
TimePeriodStart=1
TimePeriodStop=1000
NumberPerTimePeriod=Constant 0
NumberOfDirectContacts=Constant 1
DestinationType=farm
MovementDistance=1,0,0.44,0.3283,0.1367,0.055,0.011,0.029;0,0,9000,19000,29000,39000,49000,59000
ProbabilityOfTransmission=Constant 0.338
NumberPerTimePeriod[33]=Poisson .9517

[LocalSpread1]
TimePeriodStart=1
TimePeriodStop=1000
POTOffsetRelativeTo=clinical_signs
ProbabilityOfTransmission=7,1000,2000,3000;-1,0,0,0;0,0.013,0.003,0.001;1,0.039,0.009,0.003;2,0.052,0.012,0.004;3,0.052,0.012,0.004;4,0.052,0.012,0.004;5,0.052,0.012,0.004
RelativeSusceptibility[swine]=0.01

RelativeSusceptibility[sheep]=0.05
RelativeSusceptibility[goat]=0.05
RelativeSusceptibility[cattle]=1.0

[Infectivity1]
TimePeriodStart=1
TimePeriodStop=1000
TimeToClinicalSigns=Lookup
1,2,3,4,5,6,7,8,9,11,12,16,17;0,0.035,0.158,0.333,0.772,0.789,0.825,0.877,0.912,0.947,0.965,0.982,1
InfectivityRelativeTo=clinical_signs
WithinFarmSpreadProb=1.0
Infectivity[][][]=Table
1,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33;0,1,0.941,0.882,0.823,0.764,0.705,0.646,0.587,0.528,0.469,0.41,0.351,0.292,0.233,0.174,0.115,0.056,0

[Zone1]
ZoneName=ZoneCalifornia
ZoneType=explicit
IncludeEntireFarm=N
TimePeriodStartReference=simulation_start
TimePeriodStopReference=simulation_start
ChangeCount=1
TimePeriodStart1=1
TimePeriodStop1=1000
Coordinates1=.\ZoneCalUTM.txt

[Zone2]
ZoneName=Zone_ControlArea
ZoneType=radial
FarmState=in_control_area
UseFarmCentroid=Y
IncludeEntireFarm=N
ChangeCount=1
TimePeriodStart1=1
TimePeriodStop1=1000
InsideRadius1=0
OutsideRadius1=3000

[Zone3]
ZoneName=Zone_Vaccinate
ZoneType=radial
FarmState=in_vacc_zone
UseFarmCentroid=Y
IncludeEntireFarm=N

ChangeCount=1
TimePeriodStart1=1
TimePeriodStop1=1000
InsideRadius1=0
OutsideRadius1=3000

[Zone4]
ZoneName=Zone_Surv
ZoneType=radial
FarmState=in_surv_zone
UseFarmCentroid=Y
IncludeEntireFarm=N
ExcludeFarmsInZones=Zone_ControlArea
ChangeCount=1
TimePeriodStart1=1
TimePeriodStop1=1000
InsideRadius1=0
OutsideRadius1=3000

[Zone5]
ZoneName=Zone_likeDairy
ZoneType=explicit
FarmState=likeDairy
TimePeriodStartReference=simulation_start
TimePeriodStopReference=first_detection
ChangeCount=1
TimePeriodStart1=1
TimePeriodStop1=1
Coordinates1=.\ZoneCalUTM.txt

[Resource1]
ResourceName=DepopResource
WaitingFarmState=waiting_depop
ProcessingFarmState=processing_depop
CompletedFarmState=depopulated
DelayedFarmState=delayed_depop
TimePeriodToDelayedState=1
ActionOption=depopulation
FarmListOption=single_list
FarmProcessingOption=animals_per_time_period
ChangeCount=2
TimePeriodStart1=1
TimePeriodStop1=9
cattlePerTimePeriod1=2000
goatPerTimePeriod1=2000

otherPerTimePeriod1=2000
sheepPerTimePeriod1=2000
swinePerTimePeriod1=2000
TimePeriodStart2=10
TimePeriodStop2=1000
cattlePerTimePeriod2=20000
goatPerTimePeriod2=20000
otherPerTimePeriod2=20000
sheepPerTimePeriod2=20000
swinePerTimePeriod2=20000

[Resource2]
ResourceName=VaccinationResource
WaitingFarmState=waiting_vacc
ProcessingFarmState=processing_vacc
CompletedFarmState=vaccinated
DelayedFarmState=delayed_vacc
TimePeriodToDelayedState=1
ActionOption=vaccination
FarmListOption=single_list
FarmProcessingOption=animals_per_time_period
ChangeCount=2
TimePeriodStart1=1
TimePeriodStop1=9
cattlePerTimePeriod1=2000
goatPerTimePeriod1=2000
otherPerTimePeriod1=2000
sheepPerTimePeriod1=2000
swinePerTimePeriod1=2000
TimePeriodStart2=10
TimePeriodStop2=1000
cattlePerTimePeriod2=20000
goatPerTimePeriod2=20000
otherPerTimePeriod2=20000
sheepPerTimePeriod2=20000
swinePerTimePeriod2=20000

[Resource3]
ResourceName=SurvResource
ActionOption=depopulation
SurveillanceControl=Surv_ControlArea
FarmListOption=single_list
FarmProcessingOption=farms_per_time_period
ChangeCount=1
TimePeriodStart1=1

TimePeriodStop1=1000
FarmsPerTimePeriod1=0

[Depopulation1]
ControlName=Depop_Detected
ActivationOption=detected_farm
TimePeriodStartReference=simulation_start
TimePeriodStopReference=simulation_start
FarmSelectionOption=detected_farm
ActionResource=DepopResource
WaitingFarmState=waiting_depop
ProcessingFarmState=processing_depop
CompletedFarmState=depopulated
DelayedFarmState=delayed_depop
TimePeriodToDelayedState=1

[Vaccination1]
ControlName=Vacc_Zone
ActivationOption=detected_farm
TimePeriodStartReference=simulation_start
TimePeriodStopReference=simulation_start
FarmSelectionOption=zone
SelectionZone=Zone_Vaccinate
SelectionZoneFarmSortOrder=outer_to_inner
FarmClasses=31 | 32 | 33 | 51 | 53 | 73
AnimalTypes=cattle
ActionResource=VaccinationResource
WaitingFarmState=waiting_vacc
ProcessingFarmState=processing_vacc
CompletedFarmState=vaccinated
DelayedFarmState=delayed_vacc
TimePeriodToDelayedState=1
RemoveDetectedFarms=N
ImmunityFunction=Table 1,0,4,15;0,0,0.1,0.05

[Surveillance1]
ControlName=GeneralSurveillance
ActivationOption=time_period
TimePeriodStartReference=simulation_start
TimePeriodStart=1
TimePeriodStopReference=first_detection
TimePeriodStop=1
SelectionZone=ZoneCalifornia
SelectionProbability=0.65
VisitDelay=Poisson 2

VisitFrequency=Poisson 7
VisitDuration=Constant 1000
DelayToDetection=Poisson 3
DetectionRelativeTo=Clinical_signs
DetectionProbability[][][]=Constant 0.95
DetectionProbability[][][sheep]=Constant 0.5

[Surveillance2]
ControlName=GeneralSurveillance_AfterDetect
ActivationOption=time_period
TimePeriodStartReference=first_detection
TimePeriodStart=1
TimePeriodStopReference=first_detection
TimePeriodStop=1000
SelectionZone=ZoneCalifornia
SelectionProbability=0.85
VisitDelay=Poisson 2
VisitFrequency=Poisson 7
VisitDuration=Constant 1000
DelayToDetection=Poisson 3
DetectionRelativeTo=Clinical_signs
DetectionProbability[][][]=Constant 0.95
DetectionProbability[][][sheep]=Constant 0.85

[Surveillance3]
ControlName=GeneralSurv_Dairy_before
ActivationOption=time_period
TimePeriodStartReference=simulation_start
TimePeriodStart=1
TimePeriodStopReference=first_detection
TimePeriodStop=1
SurveillanceFarmState=likeDairy_beforeDetect
SelectionZone=Zone_likeDairy
SelectionProbability=0.999
VisitDelay=Poisson 1
VisitFrequency=Poisson 2
VisitDuration=Constant 1000
DelayToDetection=Poisson 3
DetectionRelativeTo=Clinical_signs
DetectionProbability[][][]=Constant 0.5

[Surveillance4]
ControlName=GeneralSurv_Dairy_after
ActivationOption=time_period
TimePeriodStartReference=first_detection

TimePeriodStart=1
TimePeriodStopReference=first_detection
TimePeriodStop=1000
SurveillanceFarmState=likeDairy_afterDetect
SelectionZone=Zone_likeDairy
SelectionProbability=0.999
VisitDelay=Poisson 0.5
VisitFrequency=Poisson 1
VisitDuration=Constant 1000
DelayToDetection=Poisson 1
DetectionRelativeTo=Clinical_signs
DetectionProbability[][][]=Constant 0.95

[Surveillance5]
ControlName=Surv_ControlArea
ActivationOption=detected_farm
TimePeriodStartReference=first_detection
TimePeriodStart=1
TimePeriodStopReference=first_detection
TimePeriodStop=1000
SurveillanceFarmState=in_control_area
SelectionZone=Zone_ControlArea
SelectionProbability=0.99
VisitDelay=Poisson 2
VisitFrequency=Poisson 3
VisitDuration=Constant 1000
DelayToDetection=Poisson 1
DetectionRelativeTo=Clinical_signs
DetectionProbability[][][]=Constant 0.99
DetectionProbability[][][sheep]=Constant 0.9

[Surveillance6]
ControlName=Surv_Zone
ActivationOption=detected_farm
TimePeriodStartReference=first_detection
TimePeriodStart=1
TimePeriodStopReference=first_detection
TimePeriodStop=1000
SurveillanceFarmState=in_surv_zone
SelectionZone=Zone_Surv
SelectionProbability=0.9
VisitDelay=Poisson 3
VisitFrequency=Poisson 7
VisitDuration=Constant 1000
DelayToDetection=Poisson 2

DetectionRelativeTo=Clinical_signs
DetectionProbability[][][]=Constant 0.99
DetectionProbability[][][sheep]=Constant 0.9

[Surveillance7]
ControlName=Surv_Trace
ActivationOption=time_period
TimePeriodStartReference=first_detection
TimePeriodStart=1
TimePeriodStopReference=first_detection
TimePeriodStop=1000
SelectionZone=ZoneCalifornia
SelectionProbability=0.75
VisitDelay=Poisson 2
VisitFrequency=Poisson 5
VisitDuration=Constant 1000
DelayToDetection=Poisson 3
DetectionRelativeTo=Clinical_signs
DetectionProbability[][][]=Constant 0.95
DetectionProbability[][][sheep]=Constant 0.85

[Tracing1]
ControlName=Tracing
TimePeriodStartReference=first_detection
TimePeriodStart=2
TimePeriodStopReference=first_detection
TimePeriodStop=1000
TracingRequired[][]=Y
ProbMovementForgotten[][]=0.2
TracingDelay[][]=Poisson 2
SurveillanceControls[][]=Surv_Trace

[MovementRestriction1]
ControlName=MovementControlControlArea
TimePeriodStartReference=first_detection
TimePeriodStart=1
TimePeriodStopReference=first_detection
TimePeriodStop=1000
MovementTypes=IDMovement_Size1 IDMovement_Size2 IDMovement_Size3 IDMovement_Size4 IDMovement_Size5 Movement_farm-market Movement_Farm_Farm_Backyard Movement_Farm_Farm_BeefL Movement_Farm_Farm_BeefS Movement_Farm_Farm_Calf_HeiferL Movement_Farm_Farm_Calf_HeiferS Movement_Farm_Farm_DairyL Movement_Farm_Farm_DairyS Movement_Farm_Farm_Goat

Movement_Farm_Farm_Sheep Movement_Farm_Farm_SwineL Movement_Farm_Farm_SwineS Movement_market-farm
SourceFarmStates=in_control_area
DestinationFarmStates=in_control_area
ProbMovementRestricted=0.99

[MovementRestriction2]
ControlName=MovementControl_Surv
TimePeriodStartReference=first_detection
TimePeriodStart=1
TimePeriodStopReference=first_detection
TimePeriodStop=1000
MovementTypes=IDMovement_Size1 IDMovement_Size2 IDMovement_Size3 IDMovement_Size4 IDMovement_Size5 Movement_farm-market Movement_Farm_Farm_Backyard Movement_Farm_Farm_BeefL Movement_Farm_Farm_BeefS Movement_Farm_Farm_Calf_HeiferL Movement_Farm_Farm_Calf_HeiferS Movement_Farm_Farm_DairyL Movement_Farm_Farm_DairyS Movement_Farm_Farm_Goat Movement_Farm_Farm_Sheep Movement_Farm_Farm_SwineL Movement_Farm_Farm_SwineS Movement_market-farm
SourceFarmStates=in_surv_zone
DestinationFarmStates=in_surv_zone
ProbMovementRestricted=0.9

[MovementRestriction3]
ControlName=StopMarkets
TimePeriodStartReference=first_detection
TimePeriodStart=2
TimePeriodStopReference=simulation_start
TimePeriodStop=1000
MovementTypes=Movement_farm-market Movement_market-farm
SourceFarmStates=!detected | detected
DestinationFarmStates=!detected | detected
ProbMovementRestricted=0.0

[Output1]
Filename=.\data_IDFW_control12_infected_0.txt
ReportType=FarmDetail
FarmDetailType=specific_state
TriggerState=infected
NumberOfColumns=3
Column1=farm_id
Column2=section_name
Column3=coordinate

[Output2]
Filename=.\data_IDFW_control12_in_control_area_0.txt
ReportType=FarmDetail
FarmDetailType=specific_state
TriggerState=in_control_area
NumberOfColumns=1
Column1=farm_id

[Output3]
Filename=.\data_IDFW_control12_in_vacc_zone_0.txt
ReportType=FarmDetail
FarmDetailType=specific_state
TriggerState=in_vacc_zone
NumberOfColumns=1
Column1=farm_id

[Output4]
Filename=.\data_IDFW_control12_in_surv_zone_0.txt
ReportType=FarmDetail
FarmDetailType=specific_state
TriggerState=in_surv_zone
NumberOfColumns=1
Column1=farm_id

[Output5]
Filename=.\data_IDFW_control12_depopulated_0.txt
ReportType=FarmDetail
FarmDetailType=specific_state
TriggerState=depopulated
NumberOfColumns=1
Column1=farm_id

[Output6]
Filename=.\data_IDFW_control12_detected_0.txt
ReportType=FarmDetail
FarmDetailType=specific_state
TriggerState=detected
NumberOfColumns=2
Column1=farm_id
Column2=section_name

;Checksum=1760877

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